Sequence:

Title:

Run on:

Searched:

Database

Result

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ppp2n.pk002.a9 Normalized Chicken Pituitary/Hypothalamus/Pineal Library (ppp2n) Gallus gallus cDNA clone ppp2n.pk002.a9 5' similar to emb|CAC34569.1 (AJ311647) avidin [Gallus gallus], mRNA sequence. BM489973.1 GI:18610904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pitutrary/Hypothalamus/Pineal Library (pgp2n)"
/sex="Male and Female"
/fissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
/dev_stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7,9)
weeks)"
                                           A1490242 EST248568
A1486930 EST24252
AW622766 EST307248
AW616209 EST307248
AW016209 EST307248
AW029928 EST285930
AJ119952 AJ319952
AJ77275 EST285930
AJ77275 EST258930
AJ77275 EST25503
AJ77275 EST25503
AJ772154 EST255503
AJ772154 EST255503
AJ772154 EST255254
B1433692 EST5465
AW039971 EST28466
AW039975 EST28466
BE53477 CC-861CL
BE628048 CC-861CL
BE628048 CC-861CL
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AI778944 EST259823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases I to 538)
Porter, T.E. and Cogburn, L.A.
Porter, T.E. and Cogburn, L.A.
ESTS from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
library, USDA/IFAFS Animal Genome Project
Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cogburn@udel.edu, www.chickest.udel.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gallus gallus"
/strain="Commercial broiler chickens"
/db_xref="taxon:9031"
/clone="pgpAn.pk002.a9"
/clone_lib="Normalized Chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. coli EMDH10B"
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BG628048
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BI435350
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B1920182 EST540117
BE922627 EST426396
B1432561 EST5322
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B143261 EST53322
B143276 EST538533
B143772 EST538533
BG600209 EST538533
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AW217469 EST296183
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BI930261 EST550150
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                                                                                                                                                                                                                                                                                                                 hits satisfying chosen parameters:
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                GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Anote—"Vector: paluescript SK(-); Site_1: EcoRI; Site_2: Xhoi; Various sizes of sprouting eyes (Zmm to 15mm) were taken from tubers. The tubers were incubated at 26c in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spernatophyta; Magnoliophyta; endicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (Dases 1 to 452)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bengyti, O., Buelli, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST505552 CSTS Solanum tuberosum CDNA clone CSTS29N13 5' Sequence,
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                                                                                                                                                                                                                                                 aacatgaccatcggggctgtgaacagcagaggtgaattcacaggcacctacatcacagcc 207
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The Institute for Genomic Research
For Clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                  144 AACATGACCATCGGGGCTGTGAACAGCAGAGGTGAATTCACAGGCACCTACATCACAGCC
                                                                                                                                                                                                                                                                                                                        gtaacagocacatcaaatgagatcaaagagtcaccattgcatgggacacaaaaacaccatc
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                                      23 others
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/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                          Indels
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                                                                                                     Ouery Match 50.2%; Score 244; DB 9; L Best Local Similarity 83.6%; Fred, No. 1.3e-58; Matches 280; Conservative 0; Mismatches 50;
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/cultivar="Kennebec"
/db_xref="taxon:4113"
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 /lab_host-"E.coli rop10
/note-"Yector: pcDNA3"
118 c 111 g 8
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/clone_lib="cSTS"
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                                      BASE COUNT
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460 bp mRNA linear EST 07-MAY-2001 pdt.pK0010.e3 chicken activated T cell cDNA Gallus gallus cDNA clone pat.pk0010.e3 5' similar to avidin, mRNA sequence.
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1 (bases 1 to 460)
Tirunagaru,V.G., Sofer,L., Cul,J. and Burnside,J.
An expressed sequence tag database of T-cell-enriched activated denomics of (2), 144-151 (2000)
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                                                                                         DB 10; Length 538;
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/db_Xref="taxon:9031"
/clone="pat.pk0010.e3"
/clone_lib-"chicken activated T cell CDNA"
/sex="male"
/cell_type="Con A-activated splenic T cell"
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Email: joan@UDel.Edu, www.chickest.udel.edu
                                                                                     Score 378.2; DB 10;
Pred, No. 9,1e-97;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE 19717, USA
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ages, Single pass
140 a 157 c 137
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University of Delaware
40 Townsend Hall, Newark,
Tel: 302 831-1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Joan Burnside
                                                                                     77.88;
96.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI980025.1 GI:5883053
                                                                                                                       Conservative
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                                                                                                     Similarity
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                                                                                                                      Matches 386;
                                                                                         Query Match
                                                                                                         Local
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Gaps

457;

Length

Score 91.2; DB 10; Pred. No. 3.6e-15;

0; Mismatches

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18.8%;
96.9%;
                                                                           Conservative
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Best Local Similarity
Matches 93; Conserv
                                     Query Match
Best Local Similarity
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BI432561
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El (bases 1 to 457)

S van der Hoeven, R., Bezzerides, J., Bachem, C., Visser, R., Karamycheva S.A., Tsal, J., Van Aken, S., Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.

Generation of ESTs from in vitro grown microtubers (2001b)

L. Unpublished (2001)

Contact: Research Genetics, Libraries Division

Tel: 1-800-711-6195

Email: cdna@resgen.com

For clone info: please contact Research Genetics, Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //note="Vector: pBluescript SK(-); Site_1: ECORI; Site_2: XhOI; Tissue supplied by Christian Bachem and Richard Visser (Department of Plant Breeding, Wageingen University, The Netherlands); sequencing by The Institute for Genomic Research. The cSTA libraries will attempt to capture the induction and initiation/initial growth of the tuber in an in vitro system as described in Bachem et al. (Plant Journal, 1996). Small microtubers develop from axillary buds attached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, cSTA (1-20) consists of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, CSTA (21-40) and cSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as P3 in Tanksley lab notebooks."
                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                               B1920182 457 bp mRNA linear EST 17-OCT-2001 EST540117 potato microtubers, in vitro-grown Solanum tuberosum cDNA clone cSTE24K6 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="Bintje"
/db_xref="taxon:4113"
/clone="cSTE24K6"
/clone=lib="potato microtubers, in vitro-grown"
/tissue_type="axillary buds of stem explants; growing sink-tubers"
                                                                                                                                  Gaps
                                                                                                                                                                        9
                                                                                                                                                                                                             61
                                                                                                                                                                      ;
0
                                                                                              Length 452;
                                                                                                                                Indels
                                                                                          Score 91.2; DB 10;
Pred. No. 3.6e-15;
0; Mismatches 3;
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/lab_host="SOLR"
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               149
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               88
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B1920182.1 GI:16216210
                                                                                        ch 18.8%;
1 Similarity 96.9%;
93; Conservative
             2 99
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Solanum tuberosum
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tubers
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Best Local Similarity
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BE922627 EST406396 potato leaves and petioles Solanum tuberosum cDNA clone cST821M15 5' sequence, mRNA sequence.

BE922627 GI:10448703
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                                                                                                                                                                                                                                                                           potato.
Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
I (bases I to 457)
I (bases I to 457)
Utterback,T., Hansen,C.L., Doan,B., Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.B., Tanksley,S.D. and Baker,B.
Upublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research For clone request: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 atggagtcaaagtttgctcacatcattgttttctttcttcttgcaactccctttgaaact 60
                            ;
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Pred. No. 3.6e-15;
0; Mismatches 3; Indels 0
                                                              /organism="Solanum tuberosum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liquid nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cathy Ronning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 18.8%;
1 Similarity 96.9%;
93; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.4%;
95.8%;
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Best Local Similarity
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BE472183
   REFERENCE
                     AUTHORS
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BI432561 452 bp mRNA linear EST 21-AUG-2001 EST535322 P. infestans-challenged leaf Solanum tuberosum CDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anote—"Vector: PBluescript SK(-); Site_1: ECORI; Site_2: XhOI; Whole plants were challenged with 450,000 sporandia/ml P. infestans US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans US-1) were used as controls and showed this sequence is actually derived from Phytophthora rather than potato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó,
                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; SpermalOphyta: Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasteridae; Solanales; Solanaceae; Solanum.

1 (bases 1 to 452)

Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B. Generation of Ests from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 89.6; DB 10; Length 452; Pred. No. 1e-14; 0; Mismatches 4; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .452
/organism="Solanum tuberosum"
/oultivar="Kennebec"
/db Arsef="taxon:4113"
/clone="PPCAS43"
/clone_ib="P. infestans-challenged leaf"
/tissue_type="leaf"
/lab_host="SOLR"
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                   PPCAS43 5' sequence, mRNA sequence. BI432561
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Best Local Similarity 95.8%;
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13F-R
                                                                                                                                      Solanum tuberosum
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                                                                                                                potato.
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EST417036 potato stolon, cornell University Solanum tuberosum cDNA clone csTA3209, mRNA sequence.
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; audicotyledons; Core eudicots;
ASteridae; cudsterids I; Solanales; Solanaceae: Solanum.

1 (bases 1 to 458)
van der Hoven,R., Bazzerides J., Bachem,C., Horvath,B., Visser,R., Holl,L.E., Lidnog,F., Hansen,T.S., Utterback,T., Bowman,C.L., Doan B., Bougri,O., Buell,C.R., Ronning,C.M., Tanksley,S.D. and Baker
1 (bases I to 457)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Ulterback, T., Hansen, C.L., Doan, B., Bougel, O., Buell, C.R., Ronning
.C.M., Fry W.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: pBlueScript SK(-); Site_1: ECOR1; Site_2:
                                                                                                                                          Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdnadresgen.com.
Location/Qualifiers
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/Clone="CSTB26K20"
/clone_lib="potato leaves and petioles"
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Contact: Research Genetics, Libraries Division Tel: 1-800-711-6195
Email: cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
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Pred. No. 1e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Organism="Solanum tuberosum"
/cultivar="Kennebec"
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/cultivar="Bintje"
/db_xref="taxon:4113"
/clone="cSTA3209"
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us-09-743-690-6.rst

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61 ctcttggcacgaaaagaaagtgatggaccagagatc 96
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1 (bases 1 to 467)

1 (bases 1 to 467)

2 Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E. and Baker, B. Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction

1 Unpublished (2000)

2 Contact: Cathy Ronning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries Division tell 1-800-711 6195, email cdna@tesgen.com

Seq primer: M13F-R.
                                                                                                                                                                            //note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; RNA was supplied by Christian Bachem & Beatrix Horvath(Laboratory of Plant Breeding, Dept. of Plant Gorices, Wageningen University, The Netherlands). Total RNA was isolated from developing axillary buds of potato nodal stem cuttings cultured on medium for the introduction of tuber formation as described in Bachem et al. (Plant Journal 1996). Tissue samples were taken of stages corresponding to growing stolons and the early stages of tuber formation."
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/clone_lib="potato stolon, Cornell University"
/tissue_type="axillary buds of stem explants, swelling
stolons"
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/tissue_type="leaf"
/dev_stage="6 week old"
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0; Mismatches
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PPCCJ81"
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                                                                                                               /dev_stage="1 to 3 days"
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                                                                                                                                                     /lab_host="SOLR"
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95.8%;
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Best Local Similarity 95.8
Matches 92; Conservative
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Solanum tuberosum
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RESULT

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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were trobers in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 bp mRNA linear EST 12-APR-2001
EST505104 cSTS Solanum tuberosum cDNA clone cSTS2818 5' sequence,
MRNA sequence.
infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than fortato." 90 g 151 t
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1 (bases 1 to 330)
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Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1.800-711-6195, email cdna@resgen.com
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1e-14;
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Pred. No. 2.7e-14;
); Mismatches 5; Indels
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/clone_lth="cSTS"
/tissue_type="sprouting eyes from tubers"
/dev_stage="l2-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                              /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
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                                                                                                                                                                              18.4%; Score 89.6; D 95.8%; Pred. No. 1e-1
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94.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              potato.
Solanum tuberosum
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LOCUS DEPINITION

RESULT 11

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BG594050

SOURCE ORGANISM

ACCESSION VERSION KEYWORDS

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Jacch Tubers:

/dev_stage="7,8 and 10 days"
/lab_host="Solk"
/lab_host="Solk"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
Xhoi; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands). The GSTA libraries will
attempt to capture the induction and initiation/initial
growth of the tuber in an in vitro system as described in
Bachem et al. (Plant Journal, 1996). Small microtubers
develop from axillary buds attached to Stem explants when
placed on a high sucrose medium (10%). Visible
morphological changes occur synchronously at day five in
the axillary buds. The first library, CSTA (1-20) consists
of axillary buds harvested on days 1-3. This targets
following libraries, CSTA (21-40) and CSTA (41-60),
capture genes involved in induction of the microtubers. The
This library is noted as P3 in Tanksley lab notebooks."

57 a 68 c 94 g 156 t
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1 (bases 1 to 490)
1 (bases 1 to 475)
van der Hoeven,R., Bezzerides,J., Bachem.C., Visser,R., Cho,J.,
Chiemingo,A., Bougri,O., Bucll,G.R., Ronning,C., Tanksley,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chlemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="axillary buds of stem explants; growing sink-tubers"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 475;
                                                                                                Generation of Ests from in vitro grown microtubers Unbublished (2001)
Contact Cathy Ronning
The Institute for Genomic Research
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/db_xref="taxon:4113"
/clone-"cgTel5N5"
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1. .475
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BG600210.1 GI:13617346
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                            AUTHORS
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EST519656 CSTE Solanum tuberosum cDNA clone csre15N5 5' sequence,
                                                                                                                                                                                                                                                                                                                                                    Sukaryota; Virial plantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Virial plantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyladons; Core eudicots; Asteridae; Solanaesa; Solanum.

1 (bases 1 to 474)

van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chlemingo, A., Boulli, C. R., Ronning, C., Tanksley, S. and Baker, B., Unpublished (2000)
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Solanum tuberosum
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
DIVISION tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
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/organism="Solanum tuberosum"
/oultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS6G18"
/clone=lib="cSTS6
/clsue_type="sprouting eyes from tubers"
/dev_stage="lg_ruly"
/lab_host="SOLR"
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Pred. No. 2.9e-14;
0; Mismatches 5; Indels
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BG594050.1 GI:13612190
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BI178711.1 GI:14644522
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source

FEATURES

TITLE JOURNAL COMMENT

REFERENCE AUTHORS Matches

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BASE COUNT ORIGIN

LOCUS DEFINITION

ACCESSION

VERSION

RESULT 12

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BI178711

SOURCE ORGANISM

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KEYWORDS

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Gaps

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Gaps

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Length 455; Indels EST 18-MAY-2001

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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University, Tanksley lab; sequencing: The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 310)
van der Hoeven, R.S., Bezzerides, J.I., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="crOBIAI5"
/clone=lib="tomato flower buds 3-8 mm, Cornell University"
/clone_lib="tomato flower buds 3-8 mm, Cornell University"
/clone="yeepe="1-6" buds"
/dev_stage="3-8mm buds"
/note="yeetor: pBlueScript SK(-); Site_1: EcoRl; Site_2:
Xhol; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrgen and then
size-separated while remaining frozen."
a 57 c 54 g 96 t
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310 bp mRNA linear EST 18-MAY-2001
EST296183 tomato flower buds 3-8 mm, Cornell University
Lycopersicon esculentum cDNA clone cTOBIA15 similar to tomato leaf
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                          Score 87; DB 10; Le
Pred. No. 5.6e-14;
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Pred. No. 7.5e-14;
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ilarity 93.8%;
Conservative (
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94.7%;
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90; Conserv
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                                                                                                                                                                                                                                                                   /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26c in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
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EST581285 potato roots Solanum tuberosum cDNA clone cPRO29K4 5' end
', mRNA sequence.
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1 (bases I to 455)
van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S., Utterback, T., Chiemingo, A., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
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The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seg primer: M13F-R.
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/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Unpublished (2001)
Contact. Research Genetics, Libraries Division
Email: 0400-711-6195
Email: cdna@resgen.com
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                                                                                                                                       1. .490
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db xref="taxon:4113"
/clone="cSTS28110"
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/db_xref="taxon:4113"
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Search completed: September 20, 2002, 15:50:02 Job time: 5311 sec

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NAME/KEY: CDS
LOCATION: 44..499
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OTHER INFORMATION:
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cgn2_6/ptodata/2/ina/5A_COMB.seq:*

cgn2_6/ptodata/2/ina/6A_COMB.seq:*

cgn2_6/ptodata/2/ina/6A_COMB.seq:*

cgn2_6/ptodata/2/ina/6B_COMB.seq:*

cgn2_6/ptodata/2/ina/FB_COMB.seq:*

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cgn2_6/ptodata/2/ina/FB_COMB.seq:*
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Compugen Ltd.
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5-09-111-752-6
5-09-111-752-8
5-09-111-752-9
5-09-371-696-1
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5-09-030-607-110
5-09-439-313-110
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US-08-554-586-1
US-08-232-43-14
US-09-100-804-1
PCT-US94-09943-1
US-09-056-012-2
US-09-042-289-1
US-09-022-238-1
US-09-022-238-1
US-09-022-238-1
US-09-022-238-1
US-09-032-238-1
US-09-135-298-3
US-09-135-988-3
US-09-135-988-3
US-09-111-752-8
US-09-111-752-9
US-09-371-696-110
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Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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APPLICANT: Kopetzki, Erhard; Muller, Rainer;
APPLICANT: Engh, Richard; Schmitt, Urban; Deger, Arno; Brandstetter, Hans
TITLE OF INVENTION: Recombinant Inactive Core
NUMBER OF SEQUENCES: 16
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peptide and 116..499 to mat peptide
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
US-09-051-696-1
US-08-026-138E-16
US-08-176-412-1
US-08-176-412-1
US-08-455-268A-1
US-08-495-695B-1
US-08-414436-1
US-08-834-655-1
US-08-834-655-1
US-08-834-655-1
US-08-814-655-1
US-08-814-2
US-08-811-2
US-08-138-641-1
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APPLICATION UNBER: DE 196 13 053.0
FILING DATE: 1-April-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 37 718.8
FILING DATE: 16-September-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6312916man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: HUBR 1105
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/831,399
1-April-1997
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; Patent No. 6312916
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREFT: 805 Third Avenue
CITY: New York City
STATE: New York
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OPERATING SYSTEM: PC-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
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TYPE: nucleic acid
STRANDEDNESS: double
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STATE: VA
COUNTRY: USA
COUNTRY: 13-0299
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  TELEFAX:
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                                                                                                                      Gaps
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                                                                     Length 604;
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TITLE OF INVENTION: COMMERCIAL PRODUCTION OF AVIDIN IN
TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                       DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 ATCAACATCTTCACTCGCCTGCGCACAGAAGGAGTGA 502
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                                                                     Score 389.4; DB 4;
Pred, No. 4.6e-118;
0; Mismatches 6;
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REFERENCE/DOCKET NUMBER: 33229/352/PIHI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K street, N.W., Suite 500
CITY: Washington
STRYE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/554,586
FILING DATE: 06-NOV-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MEYER, Terry Buclaire
APPLICANT: REGISTER III, James C.
APPLICANT: WITCHER, Derrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08554586 Patent No. 5767379 GENERAL INFORMATION:
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                                                                     Ouery Match
Best Local Similarity 98.5%;
Matches 393; Conservative
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MADDOCK, Sheila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202)672-5300
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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  US-08-831-399-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-08-554-586-1
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APPLICANT:
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100 gccagaaagtgctcgctgactgggaaatggaccaacgatctgggctccaacatgaccatc 159
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                                                                                                                                                                                                                                                                                                                                                                                             ggggetgtgaacagcagaggtgaattcacaggcacctacatcacagccgtaacagccaca 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 AGCTCCGTGAATGACATCGGCGACGACTGGAAGGCCACCCGCGTGGGCATCAACATCTTC 443
                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                Length 484;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLFOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0, Version #1.
                                                                                                                                                                                                                   Query Match 57.6%; score 279.8; DB 1
Best Local Similarity 82.7%; Pred. No. 3.4e-82;
Matches 320; Conservative 0; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CIIY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR AFPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 actcgcctgcgcacacagaaggagtga 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE. PATENTIN Release # CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TELEX: 904136,
INFORMATION FOR SED ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 484 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN CARL-HENRIK
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4978 ACAGCAGTGGAGTGGAGAAGATGACTTAGTCACAGCTCCAGCAACATATCAAATTCGA 5037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 acagcagaggtgaattcacaggcacctacatcacagccgtaacagccacatcaaatgaga 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 8040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Indels
                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31.4;
Pred. No. 4;
                                                                                                                                     APPLICATION NUMBER: US/08/596,291
FILING DATE: 09-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTOREY AGENT INFORMATION:
NAME: CAMPAGE OF THE OF THE OF T
                                                                                                                                                                                                                                                                                                                              LO461/7000
                                                                                                                                                                                                                                                                                NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFRENCE/DOCKET NUMBER: LO461
TELECOMMUNICATION INFORMATION:
TELEPAN: 617/720-3500
TELEPAN: 617/720-341
TELER: 92-174 ESEKIEL
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/09100804; Patent No. 6066472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.5%;
Best Local Similarity 57.7%;
Matches 56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 8040 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
    ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MASSACHUSETTS
COUNTRY: USA
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78..7475
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; LOCATION:
US-08-596-291-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
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US-96-291-1

Sequence 1, Application US/08596291

Sequence 1, Application US/08596291

Sequence 1, Sequence 1, EDNE

GENERAL INFORMATION:

APPLICANT: GARAS, JAN

APPLICANT: CLAESSON-WELSH, LENA

APPLICANT: HELDIN, CARL-HENRIK

TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL

TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

TITLE OF INVENTION: TYROSINE PHOSPHATASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1; Length 7218;
Pred. No. 0.055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Conservative 203; Mismatches 168;
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                                                              NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1066 ATCGCAAGCTCCCTCGACCTGCAGCCA 1040
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                                                                                                                                                              TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                    7.68;
                                                                                                                                                          (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MASSACHUSETTS
                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; IMMEDIATE SOURCE: CLONE: pTZgpt-F1s US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOSTON
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170 acagcagaggtgaattcacaggcacctacatcacagccgtaacagccacatcaaatgaga 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2 Application US/08956012
; Sequence 2 Application US/08956012
; Fatent No. 5972660
; GENERAL INFORMATION:
    APPLICANT: Hillman Jennifer
    APPLICANT: Shah, Purvi
    TTLE OF INVENTION: HUMAN HYDROXYPYRUVATE REDUCTASE
    NUMBER OF SEQUENCES: 3
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Incyte Pharmaceuticals, Inc.
    STREE: 3174 Forter Dr.
    CITY: Palo Alto
                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILIGE DATE: 01-SEP-1994
CLASSIFICATION:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTORNUE/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 teaaagagteaceattgeatgggacacaaaacaccat 266
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COMPUTER: IBM COmpatible
COMPUTER: IBM COMPATION
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Filed Herewith
                                                                                                                                                                                                                                            NAME: TWOMEY, MICHAEL J.
REGISTRATION NUMBER: P-38.349
REPERENCE/DOCKET NUMBER: LO461/7000WO
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEPHONE: 617/720-3441
    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          TELEX: 92-1742 EZEKIEL INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 8043 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SADIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskett
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78..7478
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US-08-956-012-2
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EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 acagcagaggtgaattcacaggcacctacatcacagccgtaacagccacatcaaatgaga 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.5%; Score 31.4; DB 3; Length 8040; Best Local Similarity 57,7%; Pred; No. 4; Matches 56; Conservative 0; Mismatches 41; Indels 0
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5038 CCTGGAGTTCAGCTTTGCATCAGACTCTAAGCAACAT 5074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 tcaaagagtcaccattgcatgggacacaaaacaccat 266
                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,616
REPERENCE/DOCKED NUMBER: LO461/7003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-2441
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 10.5EP-1994
ATTONNEY/ACRWT INCORMATION:
NAME: GATES, EDWARD R.
                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
                                                                                            APPLICATION NUMBER: US/09/100,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application DC/TUS9409943
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                            FILING DATE: 01-SEP-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 8040 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: 78..7475
US-09-100-804-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
APPLICANT:
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94 atccctgccagaaagtgctcgctgactgggaaatggaccaacgatctgggctccaacatg 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 954;
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APPLICANT: JEPSON, TAN
APPLICANT: SCHUCH, WOLFGANG W
TITLE OF INVENTION: PLANT-DERIVED ENZYME AND DNA SEQUENCES,
TITLE OF INVENTION: AND USES THEREOF
UNUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                 204218/SEE36438/UST
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30.8; DI
Pred. No. 2;
0; Mismatches
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COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/170,294 FILING DATE: 30-DEC-1993 PRIOR APPLICATION DATA:
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Patent No. 5866792
GENERAL INFORMATION:
                     NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REERENCE/CDCKET NUMBER: 2042
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3004
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GREENLAND, ANDREW J
APPLICANT: HOLT, DAVID C
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US-08-170-294-1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.3%;
Best Local Similarity 52.3%;
Matches 68; Conservative
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    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         LENGTH: 954 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
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Patent No. 5589614

GENERAL INFORMATION:
APPLICANT: BRIDGES, IAN G.
APPLICANT: BRIGHT, SIMON W.J.
APPLICANT: GREENLAND, ANDREW J.
APPLICANT: HALL, DAVID C.
APPLICANT: SCHUCH, WOLFGANG W.
TITLE OF INVENTION: PLANT-DERIVED ENZYME AND DNA SEQUENCES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Pred. No. 2.3;
0; Mismatches 85; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 ACCATGTGTGGGCATGACCACTTGGATGAAATCAAGAA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/170,294
FILING DATE: 30-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1100 NEW YORK AVENUE, N.W. CITY: WALLINGTON STATE: D.C. COUNTRY.
                                                                     ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0410 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1662 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB92/01187
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9114259.6
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02-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                6.48;
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Best Local Similarity 49.1%
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-956-012-2
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                                                             FILING DATE:
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TELEFAX: 202-6924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
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COUNTRY: USA
2IP: 02109
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                           linear
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HYPOTHETICAL: N
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CITY: Boston
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US-09-049-289-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 ACCACCGCCTGGTTGCGCTCGCGGCCCAGGAACGGCGAACACGCACTCCACCACGATG 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PLANT-DERIVED ENZYME AND DNA SEQUENCES TITLE OF INVENTION: AND USES THEREOF OWNESP OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSE: CUSHMAN DARBY & CUSHMAN L.L.P. STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                         NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/COCKET NUMBER: 224452/SEE36438USTD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEFAX: (202) 822-0944
TELEFAX: 6714627 CUSH
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.3%; score 30.8; DE
(2.3%; Pred. No. 2;
Ve. 0; Mismatches
                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CB92/01187
FILING DATE: 01-501-1992
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049, 289
FILING DATE:
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Patent No. 6066456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BRIDGES, IAN G.
APPLICANT: BRIGHT, SIMON W.J.
APPLICANT: GREENLAND, ANDREW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HOLT, DAVID C.
APPLICANT: JEPSON, IAN
APPLICANT: SCHUCH, WOLFGANG W.
                                                                                                                                                                                                                                                                                                                                                                                                                                   GSTII-27 - FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.3%;
Best Local Similarity 52.3%;
Matches 68; Conservative
02-JUL-1991
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                       LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: CDN/
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 gccacatcaa 223
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APPLICANT: BRIDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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COUNTRY:
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APPLICANT: Sytkowski, Arthur J. and Yang, Meiheng
TITLE OF INVENTION: A novel NFG-1 Gene that is differentially expressed in pros
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATJOANNE TOWN TOWN THE TELEPHONE TOWN TELEPHONE TOWN TELEPHONE TOWN TELEPHONE TOWN TELEPHONE TOWN THE 
APPLICATION NUMBER: US/08/170,294
FILING DATE: 30-DEC-1993
APPLICATION NUMBER: WO PCT/GB92/01187
FILING DATE: 01-JUL-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILLNS CLIASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/644,326
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9114259.6
FILING DATE: 02-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/09/022,238
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Patent No. 6177244
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSTII-27 - FIGURE 2
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Luciola cruciata
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    linear
                     MOLECULE TYPE: CORIGINAL SOURCE: ORGANISM: Luci
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TOPOLOGY: unk
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    TOPOLOGY:
                                                                                                   , NAME/KEY:
, LOCATION:
US-07-675-211-1
                                                                                    FEATURE:
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APPLICANT: KAJIXANA, NAOKI
APPLICANT: NAKANO, EIICHI
TITLE OF INVENTION: LUCIFERASE GENES, NOVEL RECOMBINANT DNAS CONTAINING THE
TITLE OF INVENTION: GENES AND A METHOD OF PRODUCING MUTANT LUCIFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 CTGGGCAGGACTGGGGGGGGGGGGATGAAGGCCCTGGGGCT 184
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/07/675,211
FILING DATE: 19910326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
              NAME: MATAVIC-MAGOVCEVIC, IVANA
REGISTRATION NUMBER: P-43,338
REFERENCE/DOCKET NUMBER: NER-262CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/07675211 Patent No. 5219737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/CDCKET NUMBER: 7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
NAME: Maravic-Magovcevic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 1644 base pairs
NUCLEIC ACID
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.3%
Best Local Similarity 56.4%
Matches 57; Conservative
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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10036
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; LOCATION:
US-09-022-238-1
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Thermostable Luciferase Of Firefly,
Thermostable Luciferase Gene Of Firefly, No. 5229285el Reco
DNA, And Process For The Preparation Of Thermostable
Luciferase Of Firefly
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    Length 1644;
                                            Indels
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COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,047
Score 30.6; DB 1;
Pred. No. 3.1;
0; Mismatches 29;
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Pred. No. 3.1;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/07903047
Patent No. 5229285
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MISICCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 7005
TELECOMMUNICATION INFORMATION:
TELEFAM: 212 790-9090
TELEFAM: 6141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kajiyama, Naoki
APPLICANT: Nakano, Eiichi
TITLE OF INVENTION: Thermost
TITLE OF INVENTION: Thermost
TITLE OF INVENTION: DNA, And
TITLE OF INVENTION: Luciferas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: CDNA to mRNA US-07-903-047-1
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Best Local Similarity 62.3%;
Matches 48; Conservative (
Query Match 6.3%;
Best Local Similarity 62.3%;
Matches 48; Conservative
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                                                                                                                                                                          83 atggaccagagatccct 99
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CLASSIFICATION: 435
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GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
ATITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1...1644
OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3%; SCOre 30.6; DB 2; 62.3%; Pred. No. 3.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOCUMENT NUMBER: PATENT NO.: 4,968,613
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JOb time: 3750 Sec
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,046A
FILING DATE: 11-25-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6680-105B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-157-046A-3/C
'Sequence 3. Application US/08757046A
'Patent No. 5976995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Seldman, Stephanle L
REGISTRATION NUMBER: 33,779
REPERENCE/DOCKET NUMBER: 666
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                       STREET: 1660 Union street
CITY: San Diego
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 02-06-96 ATTORNEY/AGENT INFORMATION:
      376 TIGGITIAGAGATACCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1644 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 619-238-09:
TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                   COUNTRY: USA ZIP: 92101-2926 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE; CDNA FEATURE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                     LUCIFERASE GENES, NOVEL RECOMBINANT DNAS CONTAINING THE GENES AND A METHOD OF PRODUCING MUTANT LUCIFERASE
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436 TIACTGTTTTCTGTACTGTTATAACTTTATCTAAGCCTTTTTAGAACTAAAATACAAFIIC 377
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                                                                                                                                                                                                                                                                       APPLICANT: KAJIYAMA, NAOKI
APPLICANT: NAKANO, EIICHI
TITLE OF INVENTION: MUTANT LUCIPERASE OF A FIREFLY, MUTANT
TITLE OF INVENTION: LUCIFERASE GENES, NOVEL RECOMBINANT
TITLE OF INVENTION: GENES AND A METHOD OF PRODUCING MUTANT
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
6.3%; score 30.6; DB 1; Length 16
Best Local Similarity 62.3%; Pred. No. 3.1;
Matches 48; Conservative 0; Mismatches 29; IndelS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7005-026-999
                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 AVENUE OF THE AMERICAS CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/675,211 FILING DATE: 26-MAR-1991
NAME: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,042
FILLING DATE: 15-JUN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MISSOCK, S. LESLIE
REGISTRATION NUMBER: 16,872
REFERENCE/DOCKET NUMBER: 7005-
TELECOMMUNICATON INFORMATION:
TELEFAX: 212-790-9090
TELEFAX: 212-790-9090
TELEFAX: 66411 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
                                                                                                                                                                                                                 Sequence 1, Application US/08076042 patent No. 5330906 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Luciola cruciata
                                                                                                    83 atggaccagagatecet 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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LOCATION: 1...
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Gaps

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Indels

29;

83 atggaccagagatecet 99

Length 1644;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

; Search time 178.23 Seconds September 20, 2002, 15:22:41 uo

(without alignments) 4681.706 Million cell updates/sec

1 atggagtcaaagtttgctca......tgcgcacacagaaggagtga 486 US-09-743-690-6 486 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3472872 Total number of hits satisfying chosen parameters:

1736436 seqs, 858457221 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| SIDSI/gcgdata/geneseq/geneseqn-emul./milg89.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:* /SIDS1/gcgdata/geneseq/genesegn-embl/NA1980.DAT:*/SIDS1/gcgdata/geneseqreembl/NA1981.DAT:*/SIDS1/gcgdata/geneseqreembl/NA1981.DAT:*/SIDS1/gcgdata/geneseqreemseqreemseqreembl/NA1982.DAT:*/SIDS1/gcgdata/geneseqreem /SIDS1/gcgdata/geneseq/genesegn-emb1/NA1988.DAT: N_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAKIES			Match Length DB ID Description	21 AAZ49865		20 AAX80197	18 AAT73194	20 AA209997	18 AAT68502	21 AAZ49854	23 AAS85309	23 ART.08242
			Length D	į	576			•				•
	æ	Query	Match	100.0	81.1	80.1	80.1	79.5	57.6	19.4	7.5	7 2
			Score	486	394.2	389.4	389.4	386.4	279.8	94.4	36.6	3.4.9
		Result	No.	1	7	3	4	S	9	7	80	σ

Resul

Drosophila melanog Drosophila melanog Cholesterol oxidas Mouse macrophage-d Mouse chemokine pr Soybaan putative c	Mouse massl cDNA m Mouse monogenic au Human colon cancer Human regulatory t Drosophila melanod	Drosophila melanog Human reproductive Human reproductive Human immune/haema Human immune/haema	immune/hae secreted p polynuclec polynuclec n A gene wi ctive intes phila melar	N. meningittdis pa Neisseria meningit N. meningittdis pa DNA encoding novel DNA encoding novel Internal control B Drosophila melanog Human full length Drosophila melanog Human GPCR protein
ABL08255 ABL08254 AAQ27956 AAX58334 AAV34998 AAA52774			∢	AAA81456 AAF21612 AAA81489 AAS77989 AAS79889 AAH48024 ABL07791 AAK94367 AAC95924 AAC85924
23 23 13 20 20 20 21		222223		
4512 6585 2385 1784 1944 2543	9436 9437 1444 2501	3042 8170 8170 9993 1503	1503 1355 2312 2376 2629 2629 8436 513445	46593 349980 837096 1414 14041 677 2544 2799 8043
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ALIGNMENTS

Potato proteinase inhibitor-I; PPI-I; streptavidin; worm; insect; plant-noxious protein; pest resistance; moth; insect; weevil; grub; beetle; fly; thrip; locust; cricket; borer; mite; looper; insecticidal; ss. Potato proteinase inhibitor-I/Avidin gene fusion sequence. BP. AAZ49865 standard; cDNA; 486 (first entry) Solanum tuberosum. 25-APR-2000 Synthetic AAZ49865; П AAZ49865 RESULT

/product= "PPI-I/Avidin fusion protein" Location/Qualifiers 1..486 /*tag= a Key

WO200004049-A1

27-JAN-2000.

99WO-NZ00110. 15-JUL-1999; 98NZ-0331002. 15-JUL-1998; (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.

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AAZ49855;
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                                                                                                                         The present sequence is the potato proteinase inhibitor-I (PPI-I)/Avidin yene fusion sequence. This encodes a chimeric polypeptide comprising Avidin mature peptide, a plant-noxious protein, fused to the ppl-I signal peptide. Transformation of plant genome with the vector carrying the gene fusion can produce pest resistance in plants, plant derived include. Stored harvest material. Pests that can be controlled include, cotton bollworm, tropical army-worm, European corn-borer or red mite, tobacco horn worm, loopers, rice stem borer, poring, outworms, diamondback moth, potato tuber moth, codling moth, indian meal moth, gypsy moth, argentine stem weevil, clover root weevil, grass-grubs, corn rootworm, rice and wheat weevils, mealworms, flour beetles, black field cricket, locusts, sawfiles, Western flower thrips, Hessian flies or
                                                                                                                                                                                                                                                                                                                                                                                                     999aaatggaccaacgatctgggctccaacatgaccatcggggctgtgaacagcagaggt 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 gggaaatggaccaacgatctgggctccaacatgaccatcggggctgtgaacagcagaggt 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 gaatteacaggeacetacateacageegtaacageeacateaaatgagateaaagagtea 240
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                                                                                                                                                                                                                                                                                                                                                                        BA;
                                                                       chimeric polypeptide and composition comprising the polypeptide iul for conferring pest resistance on plants
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                                                                                                                                                                                                                                                                                                                  Length 486;
         Markwick NP,
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                                                                                                                                                                                                                                                                                  Sequence 486 BP; 139 A; 124 C; 118 G; 105 T; 0 other;
                                                                                                                                                                                                                                                                                                                100.0%; Score 486; DB 21;
100.0%; Pred. No. 1.4e-143;
Live 0; Mismatches 0;
         Murray C,
                                                                                                        Example 2; Fig 8; 111pp; English.
         Christeller JT, Sutherland PW,
Malone LA, Burgess EPJ;
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 486; Conservative
                                       WPI; 2000-171244/15.
p-pSDB; AAY44699.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chimeric polypeptide and composition comprising the polypeptide inl for conferring pest resistance on plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1000.120
/*tag= e
/note- "Region used to design mutagenic primer"
                                                                                                  Potato proteinase inhibitor-I: PPI-I; avidin; worm; insect; plant-noxious protein; pest resistance; moth; insect; weevil; grub; beetle; fly; thrip; locust; cricket; borer; mite; looper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to design upstream primer"
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Pred. No. 1.7e-114;
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99.2%; Pred. No. ...
0, Mismatches
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/*tag= d
/note= "Region used
                                                                                                                                                                                                                                                                                                Location/Oualifiers
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/product= "avidin"
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  (first entry)
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44..499
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                                                  pCEMav avidin cDNA
                                                                                                                                                                                        insecticidal; ss.
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25-APR-2000
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Best Local S
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88 ccagagatccctgccagaaagtgctcgctgactgggaaatggaccaacgatctgggctcc 147

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AAZ49855 standard; cDNA; 576 BP.

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RESULT AA249855

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The present invention describes a fibrinogen-converting enzyme fusion protein (FCE). The fusion protein is a multidomain protein comprising:

(a) a FCE; and (b) a first member of a binding pair, that is linked to the FCE chain: (i) directly by bonds utilizing the N-terminal amino groups, the C-terminal carboxy groups or side-chain functionalities; (ii) via a bifunctional linkage motety linking the groups or functionalities; or (iii) by the first member binding to the second member of the binding pair, where the second member of the binding pair is covalantly attached to the first polypeptide chain. The FCE can be used in a method for producing fibrin. Fibrin is useful as a scalant in surgery to, e.g. reduce bleeding by scaling blood vessels, and tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       streptavidin; batroxobin; fibrinogen converting enzyme;
fusion protein; sealant; surgery; reduce bleeding; fibrin; ss.
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                           207
                        gtaacagccacatcaaatgagatcaaagagtcaccattgcatgggacacaaaacaccatc
                                                                                                                                 aacaagaggacccagcccacctttggcttcaccgtcaattggaagtttcagagtccacc
                                                                                                                                                                                     actgicticacgggccagigcticatagacaggaatgggaaggaggiccigaagaccaig
                                                                                                                                                                                                                                        tggctgctgcggtcaagtgttaatgacattggtgatgactggaaagctaccagggtcggc
                                                                                                                                                                                                                                                                                                        atcaacatcttcactcgcctgcgcacacagaaggagtga 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibrinogen-converting enzyme fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                   AAX80197 standard; cDNA; 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicken avidin encoding cDNA
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                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptavidin; biotin; anti-interference reagent; detection; mutein; avidin; non-specific binding; ss.
that have been dissected either in surgery or through wounding. The fusion protein allows for the removal of the fibringen converting enzyme from the fibrin sealant preparation via the binding of streptavidin to a biotin solid support. The present sequence encode chicken (Gallus gallus) avidin as given in the present invention.
                                                                                                                                                                                                                 aacatgaccatcggggctgtgaacagcagaggtgaattcacaggcacctacatcacagcc
                                                                                                                                                                                                                                                                                                  actgtcttcacgggccagtgcttcatagacaggaatgggaaggaggtcctgaagaccatg
                                                                                                                                                                                                                                                                                                                                        tggctgctgctgcggtcaagtgttaatgacattggtgatgactggaaagctaccagggtcggc
                                                                                                                                                                                                                                                                                                                    actgicticacgggccagigcticatagacaggaaigggaaggaggiccigaagaccaig
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0
                                                                                           Length 459;
                                                                                                               Indels
                                                             Sequence 459 BP; 118 A; 131 C; 120 G; 90 T; 0 other;
                                                                                           DB 20;
                                                                                                               9
                                                                                          Score 389.4; DB 20 Pred. No. 5.1e-113;
                                                                                                                                                                                                                                                                                                                                                                               atcaacatcttcactcgcctgcgcacacagaaggagtga 486
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                                                                                          80.1%;
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/product= a
44..115
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/*tag= c
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT73194 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biotin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wild-type avidin DNA.
                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE19637718-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
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                                                                                                              Matches 393;
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                                                                                           Query Match
                                                                                                                                   88
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us-09-743-690-6.rng

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Yla-Herttuala S,
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                                                                                                           Synthetic.
Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                       of reducing interference from non-specific binding in assays. Muttains constructed from a Strepted to a Strepted that a Strepted from a Strepted to a Strepted that a binding affinity for biotin of evidin sequence are selected that binding affinity for biotin of less than 1010 L/mole. The biotin-bindable polypeptide may be present as a polymeric conjugate, e.g. With another polypeptide or protein, especially bovine serum albumin. These muteins are used as anti-interference reagents for reducing and/or avoiding nonspecific interactions in a process for detecting an analyte. In particular, they are used in assays where the streptaviolin/avigin-biotin aperticular, they are used in assays where the streptaviolin/avigin-biotin determination of an analyte in a test Sample, e.g. a heterogeneous immunosassay or a hybridistation assay. Despite having a lower binding with native streptavidin and avidin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 aacatgaccatcggggctgtgaacagcagaggtgaattcacaggcacctacatcacagcc 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtaacagccacatcaaatgagatcaaagagtcaccattgcatgggacacaaaacaccatc 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           actgtcttcacgggccagtgcttcatagacaggaatgggaaggaggtcctgaagaccatg 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 actgretteacgggccagtgetteatagacaggaatgggaaggaggteetgaagaceatg 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tggctgctgctgcggtcaagtgttaatgacattggtgatgactggaaagctaccagggtcggc 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     occggcctctctgccagaaagtgctcgctgactgggaaatggaccaacgatctgggctcc 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 aacatgaccatcggggctgtgaacagcagaggtgaattcacaggcacctacatcacagcc 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 tggctgctgcggtcaagtgttaatgacattggtgatgactggaaagctaccagggtcggc 463
                                                                                                                                                                                             This DNA sequence encodes an avidin which is used in a novel method
                                                                                                                                 blotin - useful for reducing interference from nonspecific binding in assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptavidin and avidin muteins with reduced binding affinity for
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                              80.1%; Score 389.4; DB 18; Length 604;
                                               Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 604 BP; 164 A; 172 C; 153 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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0; Mismatches 6;
                                              Kopetzki E,
                                                                                                                                                                      Disclosure; Page 18-19; 26pp; German
                                              Engh R,
                       (BOEF ) BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ09997 standard; cDNA; 5177
96DE-1013053
                                                                                                                                                                                                                                                                                                                                                                                                                                         llarity 98.5%;
Conservative
                                               Deger A,
                                                                                WPI; 1997-482043/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
Hes 393; Conserv
                                                                                                 P-PSDB; AAW29307,
                                             Brandstetter H,
                                                           Schmitt U;
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Matches
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This invention describes a novel protein (A) which comprises a membrane-spanning domain and an extracellular domain (ECD), where the ECD comprises biotin-binding activity. Using the proteins or encoding nucleic acid molecules it is possible to target biotinylated molecules to specific sites in tissues. Molecules targeted in this way may be taken up by the tissues or cells by endocytosis, allowing the molecules to exert their effects within or on the cell. This sequence encodes a bovine scavenger receptor class A/avidin fusion protein which is used in
                                            Scavenger receptor class A, ScR, avidin, fusion protein, bovine; ECD, membrane-Spanning domain; extracellular domain; biotin-binding activity; endocytosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New fusion proteins having an extracellular domain with biotin-binding activity, used to target biotinylated molecules to specific sites in tissues -
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Bovine scavenger receptor class A (SCR)/avidin fusion protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 atcaaatgagatcaaagagtcaccattgcatgggacacaaaaacaccatcaacaagaggac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5177 BP; 1356 A; 1222 C; 1390 G; 1209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                        /product- "ScR/avidin fusion protein"
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Pred. No. 1.6e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                        Location/Qualifiers
1071..2269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the description of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kulomaa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-GB00546.
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llarity 99.7%;
Conservative
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P-PSDB; AAY03098.
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Best Local Similarity
Matches 387; Conserv
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gccaggaagtgctccctcaccggcaagtggaccaatgacctcggctccaacatgaccatc 143

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The present sequence represents a novel DNA molecule which comprises:

(a) a barley alpha amylase promoter; and (b) an optimized DNA sequence derived from the chicken avidin using a codon bias table for maize, which is operably linked to the promoter. A method has also been developed for producing avidin in commercial quantities. The method involves: (a) providing biomass (preferably seeds) from plants, of which at least certain plants contain a DNA molecule comprised of a heterologous nucleotide sequence coding for avidin, where the nucleotide sequence is operably linked to a promoter to effect expression of avidin by certain plants (e.g. the present sequence); and (b) extracting avidin from the biomass. The method can be used for the production of high levels of avidin in native conformation and active form. The constructs can also provide for high level expression of other genes.
                                               2126 gggccagtgcttcatagacaggaatgggaaggagtcctgaagaccatgtggctgctgctgcg 2185
                                                                                                                                                                                                                                                                                                                                                                Avidin; chicken; maize; transgenic plant; plant expression; barley alpha amylase signal sequence; promoter; chimeric gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence encoding avidin in plants - using a heterologous nucleotide sequence encoding avidin operably linked to a promoter to allow expression in plants
                                                                                                                                                                                                                                                                                                                                   Barley alpha amylase signal sequence and avidin chimeric gene
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                                                                                                                                  459 cactcgcctgcgcacacagaaggagtga 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Hordeum vulgare.
Chimeric - Gallus domesticus.
                                                                                                                                                                                                                                 AAT68502 standard; DNA; 484
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                                                                                                                                                                                                                                                                                                    (first entry)
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Register JC, Witcher D;
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                                                                                                                                                                                                                                                                                                  09-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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 ggggctgtgaacagcagaggtgaattcacaggcacctacatcacagccgtaacagccaca
          ggccagtgcttcatagacaggaatgggaaggaggtcctgaagaccatgtggctgctgcgg
                                                                                                                                 400 tcaagtgttaatgacattggtgatgactggaaagctaccagggtcggcatcaacatcttc
                                                                                                                                                                                 384 agctccgtgaatgacatcggcgacgactggaaggccacccgcgtgggcatcaacatcttc
                                        tcaaatgagatcaaagagtcaccattgcatgggacacaaaaacaccatcaacaagaggacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Philip
                                                                                                                                                                                                                                                                                                                                                     Potato proteinase inhibitor-I; PPI-I; avidin; worm; insect; plant-noxious protein; pest resistance; moth; insect; weevil; grub; beetle; fly; thrip; locust; cricket; borer; mite; looper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to design mutagenic primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Potato proteinase inhibitor-I"
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/note= "Region used
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Potato proteinase inhibitor-I cDNA.
                                                                                                                                                                                                                                                                           ВР
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82..103
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Malone LA, Burgess EPJ;
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                     insecticidal; ss.
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160
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AAZ49854
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100 gccagaaagtgctcgctgactggaaatggaccaacgatctgggctccaacatgaccatc 159

57.6%; Score 279.8; DB 18; Length 484; Larity 82.7%; Pred. No. 2.6e-78; Conservative 0; Mismatches 67: Indels no.

Query Match Best Local Similarity Matches 320; Conserv

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Pred. No. 2.6e-78; 0; Mismatches 67;

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ABL08242;
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                             The present sequence encodes potato proteinase inhibitor-I (PPI-I). This is used in the preparation of a binary vector designed to express a chimeric polypeptide comprising Avidin mature peptide. A plant-noxious protein, fused to the PPI-I signal peptide. The binary vector is targetted to the vacuole by PPI-I signal sequence. Transformation of plant genome with the vector can produce pest resistance in plants, plant derived products and stored harvest material. Pests that can be controlled include, cotton bollworm, tropical army worm, European corn-borer or red mite, tobacco horn worm, loopers, rice stem borer, porina, cutworms, diamondback moth, potato tuber moth, coaling moth, indian meal moth, gypsy moth, argentine stem weevil, clover root weevil, grass grubs, corn rootworm, rice and wheat waevils, mealworms, flour beetles, black field cricket, locuts, sawfiles, Western flower thrips,
                                                                                                                                                                                                                                                                                       Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                          DB 21; Length 324;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                         Sequence 324 BP; 101 A; 53 C; 68 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #21113.
                                                                                                                                                                                                                                            19.4%; Score 94.4; DB 21
99.0%; Pred. No. 9.9e-20;
tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                                                                 61 etettggeaegaaaagaaagtgatggaeeagagate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 21113; 103pp; English
                                                                                                                                                                                  Hessian flies or two-spotted mite.
          Example 2; Fig 1; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    AAS85309 standard; cDNA; 1700 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73.
P-PSDB; ABC21122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            blodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS85309;
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for restore normal activity of (II) is useful in gene therapy techniques (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensize, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        printed
from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 acaccatcaacaagaggacccagccactttggcttcaccgtcaattggaagttttcag 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 agtecaceactgtetteaegggecagtgetteatagacaggaatgggaaggaggteetga 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 aggeeteeccagecatgetgaactacaggaacacagagacgeatttggaagecagtgtgg 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 acactytyaagaaggtycettyoetteteetttyeettetyeeatgagtytaagttteatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 19208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Noté: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1700 BP; 469 A; 420 C; 427 G; 384 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.6; DB 23;
Pred. No. 0.45;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic coding sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL08242 standard; cDNA; 2781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52,38;
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 52,3
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
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P-PSDB; ABB64139.
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11-JUL-2000;
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23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL36511), expressed DNA sequences (ABL16176-ABL36511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             184 aggaatcgcaagtgtgaacagaagcagtccaaaaacttctatcaaatccgcaatgacaag 243
                                                                                                                                                                                                                                                                                                                                                         93 gatecetgecagaaagtgetegetgaetgggaaatggaecaaegatetgggetecaaeat 152
                                                                                                                                                                                                                                                                                                                                                                                    124 getgtettegaggeagtgggeaatgateegggeatggaeegettaetggeeggttetggag 183
                                                                                                                                                                                                                                                                                                                                                                                                                 153 gaccatcggggctgtgaacagcagaggtgaattcacaggcacctacatcacagccgtaac 212
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster expressed polynucleotide SEQ ID NO 19247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                 Score 34.8; DB 23; Length 2781;
Pred. No. 2.1;
0; Mismatches 82; Indels 0;
                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 19247; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 accgagagttatctacatcacacggagaccatgttgcgggacacaa 289
                                                                                                                                                                                                                                                      Sequence 2781 BP; 760 A; 590 C; 696 G; 735 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 agccacatcaaatgagatcaaagagtcaccattgcatgggacacaa
                                            NO 19208; 21pp + Sequence Listing;
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                                                                                                                                                                                                                                                                                                 Query Match 7.2%;
Best Local Similarity 50.6%;
Matches 84; Conservative
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11-JUL-2000; 2000US-0614150.
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Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical; gene;
                                                                                                                                                                              (ABB57737-ABB72072).
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                                            Claim 1; SEQ ID
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                                                                                                                               sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO. at ftp.wipo.int/pub/published_pct_sequences.
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3829 gctgtcttcgaggcagtgggcaatgatccgggcatggaccgcttactggcggttctggag 3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 gatcoctgoccagaaagtgotcgctgactgggaaatggaccaacgatctgggctccaacat 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 gaccatcggggctgtgaacagcagaggtgaattcacaggcacctacatcacagccgtaac 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster expressed polynucleotide SEQ ID NO 19244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
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0
                                                                                                                                                                                                                                                                                                                            Length 4512;
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                                                                                                                                                                                                                                                             Sequence 4512 BP; 1395 A; 1027 C; 1192 G; 898 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3949 accgagagttatctacatcacacggagaccatgttgcgggacacaa 3994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 agccacatcaaatgagatcaaagagtcaccattgcatgggacacaa
                                                                                                                                                                                                                                                                                                                        Score 34.8; DB 23;
Pred. No. 2.7;
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                                                                                                                                                                                                                                                                                                                            7.2%;
50.6%;
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
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pharmaceutical; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
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Matches 84; Conserv
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This nucleotide sequence encodes murine MDC (see AAY05876), a novel macrophage derived C-C chemokine. Murine MDC cDNA was isolated from a mouse thymus cDNA library using rat MDC cDNA (see AAX58335) as probe. Murine MDC competes with human MDC for binding to human CCR4. The invention provides vertebrate MDC polypeptides (see also AAV05871, AAY05877 and AAV05880) and isolated polynucleotides encoding them, as well as vectors, host cells and methods for the recombinant or synthetic production of MDC. Also provided are MDC analogues, antibodies and antagonists. The MDC antagonists are used for the preparation of medicaments for the suppression of the
                                                                                                                                                                                                                        284 ccaccitiggciticaccgicaatiggaagititicagagitccaccactgiciticacgggcc 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrate Macrophage Derived Chemokines, analogues and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDC; macrophage derived chemokine; C-C chemokine; mouse; antagonist, chemoattractant; antiproliferative, dermatological; immunosuppressive; antiinflammatory; antiasthmatic; antiaggregant; asthma; allergy; HIV; infection; lupus erythematosus; therapy;
                                                                                                                                                                                                                                                                                                                                                                344 agtgottoatagacaggaatgggaaggaggtootgaagaccatgtggotgctg 396
                                                                                                     Length 2385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Raport CJ;
                                                                                                                                                              Indels
                         Sequence 2385 BP; 448 A; 829 C; 733 G; 375 T; 0 other;
                                                                                                                                                              46;
                                                                                                             DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse macrophage-derived C-C chemokine MDC cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gray PW,
                                                                                                       score 34.6; DB
Pred. NO. 2.3;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godiska R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                          7.18;
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                                                                                                          Query Match 7.1
Best Local Similarity 56.6
Matches 64; Conservative
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73..276
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..279
/*tag=
1..72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ICOS-) ICOS CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chantry DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; ss.
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SO
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                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                       (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4962 aggaatcgcaagtgtgaacagaagcagtccaaaaacttctatcaaatccgcaatgacaag 5021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 gaccatcggggctgtgaacagcagaggtgaattcacaggcacctacatcacagccgtaac 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 gatecetgecagaaagtgetegetgaetgggaaatggaceaaegatetgggeteeaaeat 152
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of the cholesterol oxidase gene from Brevibacterium sterollcum which can be used in the recombinant preparation of cholesterol oxidase at high purity and low cost in Streptomyces spp. pref. S.lividans CHS31. See also AAQ27957-Q27959.
                         insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL36511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prepn. of cholesterol oxidase (I) – using microbe belonging to Streptomyces genus holding recombinant DNA of specified sequence
                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                   Length 6585;
                                                                                                                                                                                                                                                  Sequence 6585 BP; 1938 A; 1457 C; 1687 C; 1503 T; O other;
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 agocacatcaaatgagatcaaagagtcaccattgcatgggacacaa 258
                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                Score 34.8; DB 23;
                                                                                                                                                                                                                                                                                                                                                                   3.3
                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 9; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ27956 standard; DNA; 2385 BP
                                                                                                                                                                                                                                                                                                                             7.28;
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617..751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxidase gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP04210592-A.
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                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                     346 tgcttcatagacaggaatgggaaggaaggtcctgaagaccatgtggctgctgcggtcaagt 405
                                                                                                                                                                                                                      Chemokine; human; detection; forensic; diagnostic; treatment; cancer; degenerative condition; abnormal proliferation; regeneration; degeneration; atrophy; ss.
                                                                                                                                                                               Gaps
proliferation of a mammalian immunodeficiency virus, for inhibiting
           platelet aggregation in a mammal, for the treatment or palliation of lupus erythematosus in a mammal, for inhibiting MDC-induced activation, chemotaxis or proliferation of cells that express the chemokine receptor CCR4, for inhibiting or palliating an allergic reaction in a mammal, and for treating asthma (all claimed). MDC polypeptides are also used in claimed vaccine compositions.
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9
                                                                                                                                                    Score 33.8; DB 20; Length 1784;
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                                                                                                                                                                             17; Indels
                                                                                                          Sequence 1784 BP; 412 A; 501 C; 410 G; 459 T; 2 other;
                                                                                                                                                                 Pred. No. 3.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
/product= 331D5
/note= "chemokine protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
165..443
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse chemokine protein 331D5 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zlotník A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 79-80; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer and degenerative conditions
                                                                                                                                                                                                                                                                                                                                                       AAV34998 standard; cDNA; 1944 BP
                                                                                                                                                 7.0%;
72.1%;
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                                                                                                                                                               Local Similarity 72.1 tes 44; Conservative
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237..440
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165..236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-207387/18
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                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
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                                                                                                                                                    Query Match
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diagnostics. The chemokines themselves are useful for treatment of, e.g. cancer or degenerative conditions. Abnormal proliferation, regeneration, degeneration or atrophy may be treated by the inventive compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               carbon catabolite repression; sucrose non-fermenting protein 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Soybean putative catabolite repression protein SNF1 coding sequence #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins involved in carbon catabolite repression in plants and seeds, useful for controlling carbon and nitrogen partitioning pathways during plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maccol DJ;
                                                                                                                                                                   346 tgcttcatagacaggaatgggaaggaggtcctgaagaccatgtggctgctgcggtcaagt 405
                                                                                                                                                                                             424 tactccataaactgtcctagggaggaggacctgatgaccatgggtctggtggtccagg 483
                                                                                                                                         Gaps
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                                                                                                         Length 1944;
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                                                                                                                                         Indels
                                                           Sequence 1944 BP; 459 A; 531 C; 454 G; 500 T; 0 other;
                                                                                                       Score 33.8; DB 19;
Pred. No. 3.7;
                                                                                                                                     17;
                                                                                                                                       0; Mismatches
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73..1620
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 47-48; 59pp; English.
                                                                                                                                                                                                                                                                                                                                      AAA52774 standard; cDNA; 2543 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "SNF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                         7.08;
                                                                                                                       72.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US29824
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                                                                                                                                       44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allen SM, Heppard EP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNF1; plant growth; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth and development
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                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAB03422.
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Search completed: September 20, 2002, 16:25:08 Job time: 3747 sec

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AJ311647 Gallus ga 221536 G.gallus av 221535 G.gallus av 222883 G.gallus av 222883 G.gallus av 222883 G.gallus av 222883 G.gallus av 237053 Gallus gal AJ237659 Gallus gal AJ21616 G.gallus av AJ311648 Gallus ga LO617 Solanum tub LO605 Solanum tub K67675 S.tuberosum K67675 S.tuberosum K67675 S.tuberosum K67675 S.tuberosum K67675 S.tuberosum K67675 S.tuberosum K67675 Solanum tub K67675 S.tuberosum K67675 S.tuberosum K67675 S.tuberosum

L27818 Gallus gall

K05343 Chicken mRN

A93651 Sequence 3 AR177253 Sequence AX018983 Sequence

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chicken.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Location/Qualifiers
1. 604
/organism="Gallus gallus"
/db_xref="taxon:9031"
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Z12619 N.tabacum P X67075 N.tabacum T AF429315 Homo sapi

Homo sapi

VRT 21-MAR-1995

Beattie, W.G.,

source

Description

Query Score Match Length DB

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Brandstetter,H.
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Sequence 3 from patent US 6312916.
AR177253 GI:17919608
                                                /organism="unidentified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                 /note-"pot.alternative rRNA binding site"
44. .502
/note-"precursor polypeptide (AA -24 to 128)"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 604;
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/tissue_type="oviduct (laying hen)"
/clone_lib="lambda gtl1"
                                                                                                                                                                                                                                                                       116. .499
/product="mature avidin (AA 1-128)"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 389.4; DB 5;
Pred. No. 1e-109;
0; Mismatches 6;
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                                              /note="pot.rRNA binding site"
                                                                                                                                   /codon_start-1
/protein_ld="CAA28954.1"
/db_xref="G1:63072"
/db_xref="Swiss-PROT:P02701"
                                                                                                                                                                                                                                                                                                                                                                        115
                                                                                                                                                                                                                                                                                                     565, .570
/note="pot.polyA signal"
584
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A93651
A93651.1 GI:6741840
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172 c 153 g
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unclassified.
1 (bases 1 to 604)
Mueller,R.D. and Deger,A.D.
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Best Local Similarity 98.5
Matches 393; Conservative
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/transl_table=11
/protein_id="Cac07722.1"
/db_xref="GI:0043079"
/translation="MAQWDDFPDQQEDTDSCTESVKFDARSVTALLPPHPKNGPTLQE
RMKSYKTALITLYLIVEVVLVPIIGIVAAQLLKWETRNCTVGSVNADISPSPEGKGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLSSIOEHENIIGDISKSLVGLÄTTVLDLOFSIETLAGRVOENAFKÖOEEMRKLEERI
YNSAEIKREDEKQYLEGOERKGEMKLLNIITUBLRLKDWEHSGTLKRTLLOGARKC
SLIGKWTNDLGSNWIIGAVUSRGEFFGTY TRAVTATSNEIKESPLAGTONTINKRTOP
TFGFTVWWKFSESTTVFTGQCFIDRNGKEVLKTWWLLRSSVNDIGDDWKATRVGINIF
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Biotin-binding receptor molecules
Biotin-binding receptor molecules
Patent: WO 9942577-A 1 26-AUG-1999;
YLA HERTTUALA SEPPO (FI); AIRENNE KARI (FI); KULOMAA MARKKU (FI);
MARJOMAKI VARPU (FI); LEHTOLAINEN PAULLINA (FI); EUROGENE LIMITED (GB)
                                                                                                                207
                                                                                                                                                                                                                               267
                                                                                                                                                                                        387
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synthetic construct
artificial sequence.
1 (bases 1 to 5177)
Yla Herttuala, S., Airenne, K., Kulomaa, M., Marjomaki, V. and
                                                                                                                148 aacatgaccatcggggctgtgaacagcagaggtgaattcacaggcacctacatcacagcc
                                                                                                                                                                        208 gtaacagccacatcaaatgagatcaaagagtcaccattgcatgggacacaaaacaccatc
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 Length
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                               Indels
Score 389.4; DB 6;
Pred. No. 1e-109;
0; Mismatches 6;
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1. .5177
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Designed DNA sequence to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1071. .2273
/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                      464 ATCAACATCTTCACTCGCCTGCGCACACAGAAGGAGTGA
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80.1%;
98.5%;
                               Conservative
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              Best Local Similarity
                            Matches 393;
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7875; avidin; primer; sequence tagged site.
Gallus gallus (strain White Leghorn, sub_species domesticus) female adult oviduct DNA.
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Gallus gallus (clone 44) STS, avidin gene, complete cds, sequence
tagged site.
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
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                                                                                                                                                                                                                                                                                                                                                                  219 atcaaatgagatcaaagagtcaccattgcatgggacacaaaaacaccatcaacaagaggac 278
                                                                                                                                                                                    tyccagaaagtyctcyctyactyygaaatyyaccaacyatctyyygctccaacatyaccat 158
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                                                                                          Length 5177;
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Sequence of the chicken egg-white avidin gene
Unpublished (1994)
                                                                                        Score 386.4; DB 6;
Pred. No. 1.4e-108;
                                                                                                                                     0; Mismatches
  1208
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/strain="White Leghorn"
/sub_species="domesticus"
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1221
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1359
BASE COUNT
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(bases 1 to 1224)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="AVD"
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/gene="AVD"
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/gene="AVD"
/number=2
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410 C
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/gene="AVD"
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/gene="AVD"
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                                                                                                                                                                                            /translation-"myhatsplililislalvapsisarksligkwyndlgsnmti
GAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTINKRTQPTFGFTVNWKFSESTTV
FTGQCFIDRNGKEVLKTWMLLRSSVNDIGDDWKATRVCINIFTRLRTQKE"
                                                                                                                                                                                                                                                                    /note="corresponds to position 107 in the cDNA; a possible
                                                                                                                                                                                                                                                                                                                                                                   /note-"the gene and the cDNA encode for glutamine whereas the protein sequence has a glutamic acid at this position" /citation=[1]
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                                                                 /note="30 cycles (94C 1 min, 55C 1 min, 72C 1.5 min), Tag
pol, 1119 bp"
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 tgaacagcagaggtgaattcacaggcacctacatcacagccgtaacagccacatcaaatg 226
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                                                                                                                           .934,1022. .1067)
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Gallus gallus AVD gene for avidin, exons 1-4.
AJ311647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                              PCR error in the gene sequence"
/Citation=[2]
/replace="g"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 211.4; DB Pred. No. 2e-54; 0; Mismatches
                                                                                                       /note="PCR; putative"
join(13. :93,178. :388,814.
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243
                                                                                                                                                     /product-"avidin"
/protein_id="AAB59733.1"
/db_xref-"GI:451889"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1044. .71117
complement(1100. .1119)
                       /tissue_type="oviduct"
/dev_stage="adult"
1. .1119
/db_xref-"taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PCR; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 g
                                                                                                                                                                                                                                                                                                                                                                                                              /replace-"gar"
389. .813
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AVD gene; avidin.
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Best Local Similarity 99.5%;
Matches 212; Conservative C
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325. .327
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Gallus gallus
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ACCESSION
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ORIGIN
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2 (bases I to 1224)
Ahlroth, M.K., Kolda, E.H., Ewald, D., Masabanda, J., Sazanov, A.,
Fries, R. and Kuloma, M.S.
Characterization and chromosomal localization of the chicken avidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /goin_start-1
/product="avidin"
/protein_id="CAC34569.1"
/db_xref="c1:13397826"
/translation="mWHATSPLILLILSLALVAPGLSARKCSLTGKMDNDLGSNMTI
GAVNSKGEFGTYTTATATATSREIKESPLHGTONTINKTQPTFGFTYWWKFSBSTTY
FTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVGINIFTRLRTOKE"
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                                                                                                                                                                                                                                                                                                                                         Submitted (09-MAR-2001) Ahlroth M.K., Department of Biological and Environmental Science, University of Jyvaskyla, PO Box 35, FIN-40351 Jyvaskyla, FINLAND LOCALION/Qualliflers
Wallen, M.J., Laukkanen, M.O. and Kulomaa, M.S.
Cloning and sequencing of the chicken egg-white avidin-encoding
gene and its relationship with the avidin-related genes Avri-Avrs
Gene 161 (2), 205-209 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 ctgccagaaagtgctcgctgactgagaaatggaccaacgatctgggctccaacatgacca 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96. 1152
/gene="AVD"
join(-698. 178, 263. .473,899. .1019,1107. .>1152)
/gene="AVD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .473,899. .1019,1107. .1152)
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                                                                                                                                                                                                                   Anim. Cenet. 31 (6), 367-375 (2000) 21070478
                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1224
/organism-"Gallus gallus"
/db_xref-"taxon:9031"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257
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join(98. .178,263.
/gene="AVD"
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/gene="AVD"
/number=3
1107, 1152
/gene="AVD"
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BEST LOCAL Similarity 94.6%;
Matches 210; Conservative (
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Ahlroth, M.K.
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97

VRT 03-FEB-1994

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2 (bases 1 to 277)
Keinanen, R.A., Wallen, W.J., Kristo, P.A., Laukkanen, M.O.,
Toimela, T.A., Helenius, M.A. and Kulomaa, M.S.
Molecular cloning and nucleotide sequence of chicken avidin related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae; Gallus.

1 (bases 1 to 277)

Kunnas, T.A., Wallen, M.J. and Kulomaa, M.S.

Induction of chicken avidin and related mRNAs after bacterial
                                                                              | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 | 139 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-FEB-1993) Wallen M. J., University of Tampere,
Department of Biomedical Sciences, Tampere, Finland, SF-33101
Location/Qualifiers
                                                                                                                                                                                                            GGAVR2MRN 277 bp mRNA linear VF
G.gallus avr2 mRNA for avidin related gene 2, partial.
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/organism="Gallus gallus"
/strain="White Leghorn"
/db_xref="taxon:9031"
/sex="Female"
/dev_stage="immature, estradiol treated"
/tissue_type="oviduct"
/clone="poAVR2-f1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="avr2"
/standard_name="Avidin related gene 2 |
/citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1216 (3), 441-445 (1993)
94092737
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                                                                                                                                                                                                                                                                                                                459 cactcgcctgcgcacacagaaggagtga 486
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81.8%;
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72 c
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Wallen, M.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z21535.1 GI:65428 avidin; avr2 gene.
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Best Local Simi
Matches 180;
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GGAVR2MRN
LOCUS
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TITLE
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MEDLINE
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JOURNAL
                            38
                                                                              339
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KEYWORDS
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Submitted (01-FEB-1993) Wallen M. J., University of Tampere,
Department of Biomedical Sciences, Tampere, Finland, SF-33101
2 (bases 1 to 277)
Keinanen, R.A., Wallen, M.J., Kristo, P.A., Laukkanen, M.O.,
Toimela, T.A., Helenius, M.A. and Kulomaa, M.S.
Molecular cloning and nucleotide sequence of chicken avidin related
                                                                                                                                                                                                                                                                                                                                                                                                                                         VRT 16-DEC-1997
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1 (Sases 1 to 277)
Wallen, M.J.
Direct Submission
                                                                                                                                                     CTTCGTCACAGTGCTCGCTGACTGGGAAATGGGACAACGACCTGGGCTCCAACATGACCA 311
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Kunnas,T.A., Wallen,M.J. and Kulomaa,M.S.
Induction of chicken avidin and related mRNAs after bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                            ьсамиямки 277 bp mRNA linear VR
G.gallus avr3 mRNA for avidin related gene 3, partial.
Z21536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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/tissue_type="intestine"
/clone="pcAVR3-f1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 1216 (3), 441-445 (1993) 94092737
                                                                                                                                                                                                                                                         DB 5;
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/strain="White Leghorn"
/db_xref="taxon:9031"
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/replace="t"
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REFERENCE

SOURCE

AUTHORS

TITLE

REFERENCE

JOURNAL

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FEATURES

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0
                              Score 156; DB 5; Length 277;
Pred. No. 2.3e-37;
0; Mismatches 40; Indels
55
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279 ccagcccacctttggcttcaccgtcaattggaagttttcagagtccaccactgtcttcac 338

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VRT 18-MAR-2001
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[ (bases 1 to 1334)
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Molecular Cloning of three structurally related genes for chicken
avidio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 ACATCAAGCTATCACCACTGCTTGGGATCCAACA-----CAAAAGAGCCTGCCAGCCCA 349
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            /standard_name-"Avidin related gene 3"
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                            /note="putative exons 1-4'
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complement(1094. .1113)
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386 c 288 g
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365
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/replace="g"
                                                           /citation-[1
                                                                                         178. .382
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avidin; avr4 gene.
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2 (bases 1 to 1133)
2 keinanen, R.A., Wallen, W.J., Kristo, P.A., Laukkanen, M.O.,
Toimela, T.A., Helenius, M.A. and Kulomaa, M.S.
Molecular cloning and nucleotide sequence of chicken avidin-related
genes 1-5
                                                                                                                                                                                                                                                VRT 20-JUN-1997
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Pastaninae; Gallus.
1 (Dases 1 to 1133)
Keinanen, R.A., Laukkanen, M.L. and Kulomaa, M.S.
Molecular cloning of three structurally related genes for chicken
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/dev_stage="adult"
/tissue_type="oviduct"
/clone_lib-"genomic library (EMBL4) of Bert W. O'Malley"
/clone="pgAV3.3 (249-1133)"
<1. 93
                                                                        STS feature; 30 cycles (94C 1 min, 55C 1 min, 72C 1.5 min), Tag pol, 1113 bp*
                                cactgicticacgggccagigcticatagacaggaatgggaaggaggtcctgaagaccat 386
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Submitted (01-FEB-1993) Wallen M. J., University of Tampere,
Department of Biomedical Sciences, Tampere, Finland, SF-33101
Location/Qualiflers
1. 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunnas,T.A., Wallen,M.J. and Kulomaa,M.S.
Induction of chicken avidin and related mRNAs after bacterial
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join(<1. .93,178. .382,808. .928,1016. .>1133)
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join(1. .93,178. .382,808. .928,1016.
/gene="avr3"
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/strain="White Leghorn"
/db_xref="taxon:9031"
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Wallen, M.J.
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Gallus gallus
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2 (bases 1 to 1334)
Keinanen, R.A., Wallen, M.J., Kristo, P.A., Laukkanen, M.O.,
Toimela, T.A., Helenius, M.A. and Kuloma, M.S.
Molecular cloning and nucleotide sequence of chicken avidin-related
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Keinanen, R.A., Wallen, W.J., Kristo, P.A., Laukkanen, M.O.,
Toimela, T.A., Helenius, M.A. and Kulomaa, M.S.
Molecular cloning and nucleotide sequence of chicken avidin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRT 18-MAR-2001
                                                                                                                                                                                                                                                                                                                              /sex="Female"
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join(<177. 294,379. 583,1009. 1129,1217. >1334)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         497 ACATCACGCTATCACCACTGCTTGGGATCCAACA-----CAAAAGAGCCAGCCAGCCCA 550
                                                                                                                                             Vallen, M.J.

Direct Submission
Submitted (04-JUN-1993) Wallen M. J., University of Tampere,
Department of Biomedical Sciences, Tampere, Finland, SF-33101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1129,1217. .1334)
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Gallus gallus mRNA for avidin related protein 1, partial
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Pred. No. 3.4e-29;
0; Mismatches 38;
                                                                                              genes 1-5
Bur. J. Biochem. 220 (2), 615-621 (1994)
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/organism="Gallus gallus"
/strain="White Leghorn"
/db_xref="taxon:9031"
/clone="pgAV2H52"
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join(177. .294,379.
/gene="avr5"
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Best Local Similarity 79.3%;
Matches 169; Conservative
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Gallus gallus
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                                                                                                                              94170814
 88260103
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                    sites)
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KEYWORDS
SOURCE
ORGANISM
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   MEDLINE
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                                                  AUTHORS
                                                                                                                  JOURNAL
                                                                                                                                 MEDLINE
                                                                                                                                                  REFERENCE
                                                                                                                                                                   AUTHORS
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                                                                                TITLE
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                              2 (bases 1 to 1334)
Keinanen, R.A., Wallen, M.J., Kristo, P.A., Laukkanen, M.O.,
Toimela, T.A., Helenius, M.A. and Kulomaa, M.S.
Molecular cloning and nucleotide sequence of chicken avidin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
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                                                                                                                                                                                                                                                                                                                                           /tissue_type="oviduct"
//clone_lib="genomic library (EMBL4) of Bert W. O'Malley"
//dev_stage="adult"
join(<177. 294,379. 583,1009. 1129,1217. >1334)
//stene="avrt"
//standard_name="Avidin related gene 4"
/note="putative exons 1-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1334)
Keinanen, R.A., Laukkanen, M.L. and Kulomaa, M.S.
Molecular cloning of three structurally related genes for chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agtgctcgctgactgggaaatggaccaacgatctgggctccaacatgaccatcggggctg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 AGTGCTCGCTGACTGGGAAATGGACCAACAACCTGGGCTCCATCATGACCATCAGGGCTG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                           Direct Submission
Submitted (04-JUN-1993) Wallen M. J., University of Tampere,
Department of Biomedical Sciences, Tampere, Finland, SF-33101
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agatcaaagagtcaccattgcatgggacacaaaaacaccatcaacaagaggacccagccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /citation=[2]
join(177. .294,379. .583,1009. .1129,1217. .1334)
/gene="avr4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 130.2; DB 5; Length
Pred. No. 3.4e-29;
0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                        Eur. J. Biochem. 220 (2), 615-621 (1994)
94170814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .1334 /
/organism="Gallus gallus"
                                                                                                                                                                                                                                                                           /strain="White Leghorn"
/db_xref="taxon:9031"
/clone="pgAV2H48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1334 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G.gallus avr5 gene, exons 1-4. 222882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 g
                                                                                                                                                                                                                                                                                                                              /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.8%;
Best Local Similarity 79.3%;
Matches 169; Conservative
                                                                                                                                         3 (bases 1 to 1334)
Wallen, M.J.
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                                                                                                 genes 1-5
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88260103
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                  (sites)
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GGAVR5X14
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                REMARK
REFERENCE
                                               AUTHORS
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Gaps

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/LTBDSlbtion="MYHATSPLLLLLLSLALVAPGLSARKCSLTGEMDNNLGSNMTI
GAVNDNGEFNGTYITAVADNPGNIKLSPLLGIQHKRACQPTFGFTVHWNFSESTSVFV
GQCFIDRSGKEVLKTKWLQRLAVDDISDDWRATRVGYNNFTRQRTVEE"
     Characterization and chromosomal localization of the chicken avidin
                                                                                                 Direct Submission
Submitted (22-MAR-1999) Ahlroth M.K., Department of Biological and
Environmental Science, University of Jyvaskyla, PO Box 35,
FIN-40351 Jyvaskyla, FINLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 ctgccagaaagtgctcgctgactgggaaatggaccaacgatctgggctccaacatgacca 157.
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/gene="avr?"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1061)
                                                                                                                                                                                                                                                                                                                          /clone_lib-"gridded genomic cosmid library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="avidin-related protein 7 (AVR7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="avidin-related protein 7 (AVR7)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref-"SWISS-PROT: P56736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(13. .93,178. .382,808.
/gene="avr7"
                                                                                                                                                                                                                                                                                                                                                                                              .382,808.
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                                                                                                                                                                                                 /organism="Callus gallus"
/strain="Rhode Island"
/db_xref="taxon:9031"
/chromosome="2"
                                    Genet. 31 (6), 367-375 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAB39894.1"
/db_xref="G1:4539030"
                                                                                                                                                                          Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                            join(<1. .93,178.
                                                                                                                                                                                                                                                                                         /clone="C21-154"
/sex-"female"
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                                                                                                                                                                                                                                                                          /map="q16-q21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "avr7"
                                                                                                                                                                                                                                                                                                                                                           /gene-"avr7"
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1016. .1133
/gene="avr7"
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/qene="avr7"
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1124. .1129
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                                                                2 (bases 1 to 1133)
Ahlroth,M.K.
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929. .1015
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383. .807
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/gene="av
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                                                                                                                                                                          FEATURES
                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT:013153"
/translation="STSVFVGQCFVDKSGKEVLKTKWLORLAVDDISDDWKATRVGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                          Submitted (18-JUN-1997) Kulomaa M.S., Department of Biological and Environmental Science, University of Jyvaskyla, PO Box 35 FIN-40351 Jyvaskyla FINLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRT 13-FEB-2001
2 (bases 1 to 170)
Wallen, M.J., Laukkanen, M.O. and Kulomaa, M.S.
Cloning and sequencing of the chicken egg-white avidin-encoding gene and its relationship with the avidin-related genes Avrl-Avr5 95394357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken.
Gallus gallus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves; Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
1 (bases 1 to 1133)
Ahlroth,M.K., Kola,E.H., Kulomaa,M.S., Ewald,D., Masabanda,J.,
Sazanov,A. and Fries,R.
                                                                                                                                                       Lappalainen, P., Kunnas, T., Punnonen, E.L. and Kulomaa, M.S. Expression of the avidin and avidin-related gene 1 in the chicken macrophage cell-line HD11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 agtecaccactgtetteaegggeeagtgetteatagaeaggaatgggaaggaggteetga 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 agaccatgtggctgctgcggtcaagtgttaatgacattggtgatgactggaaagctacca 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AGACCAAAAFGCCTGCAACGCTTAGCAGTTGATGACAATAGTGATGACTGATGAAGCTACCAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"avidin related protein 1"
/protein_id="CAB09798.1"
/db_xref-"GI:2226408"
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AJ237659
AJ237659.1 GI:4539029
avidin-related protein 7 (AVR7); avr7 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 125.4; DB 5;
Pred. No. 6.4e-28;
0; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                                             /organism-"Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                             /strain-"White Leghorn"
/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                   111_type="macrophage".
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Kulomaa,M.S.
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Matches 141; Conservative
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/gene="avrl"
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Keinanen, R.A., Wallen, M.J., Kristo, P.A., Laukkanen, M.O.,
Toimela, T.A., Helenius, M.A. and Kulomaa, M.S.
Molecular cloning and nucleotide sequence of chicken avidin-related
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join(*177. . 294,379. . 583,1010. .1130,1218. .>1335)
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/citation=[1]
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                                                                           167 CTTCGTCACAGTGCTCGCTGACTGGGGAATGGGACAACAACCTGGGGTCCCAACATGACCA 226
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                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to Laukanen, M.L. and Kulomaa, M.S.
Molecular cloning of three structurally related genes fo
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/gene="avrl"
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/gene="avrl"
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/organism="Gallus gallus"
/strain="White Leghorn"
/db_xref="taxon:9031"
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/sex="Female"
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1010. .1130
/gene="avr1"
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1218. .>1335
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Wallen, M.J.
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221611.1 GI:65431
avidin; avrl gene.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases I to 113)

Ahlroth, M.K., Kola, E.H., Ewald, D., Masabanda, J., Sazanov, A., Fries, R. and Kulomaa, M.S.
Characterization and chromosomal localization of the chicken avidin
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Submitted (22-MAR-1999) Ahlroth M.K., Department of Biolog
Environmental Science, University of Jyvaskyla, PO Box 35,
FIN-40351 Jyvaskyla, FINLAND
Location/Qualifiers
1. 1133
/organism="Galua"
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/chromosome="2"
                                                                                                                     ;
9
                                                                                   Length 1335;
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avidin-related protein 6 (AVR6); avr6 gene.
                                                                                   DB 5;
                                                                                 Score 118.4; DB 5
Pred. No. 1.6e-25;
0; Mismatches 51
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/gene="avr6"
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74.38;
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Ahlroth, M.K.
              433 c
/number=4
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Best Local Similarity 74.3
Matches 165; Conservative
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Gallus gallus
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                                                                                                                                           'product-"avidin-related protein 6 (AVR6)"
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/number-2
/gene="avr6"
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/gene="avr6"
/number-3
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1124. .1129
/gene="avr6"
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/gene="avr6"
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Search completed: September 20, 2002, 16:20:58 Job time: 5557 sec

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Q07459 solanum tub
Q43648 solanum tub
Q43651 solanum tub
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Q41490 solanum tub
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Q91844 arabidopsis
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Match Length DB
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Perfect score:
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091gt4 oryza sativ 09w0f6 drosophila P91151 caenorhabdi 035317 mus musculu 060264 rattus norv 060280 homo sapien 008835 cercopithec 013854 schizosacch 09rkq8 streptomyce 09can8 arabidopsis 05gan8 arabidopsis 05gan9 arabidopsis	00
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ALIGNMENTS

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01-NOV-1996
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043651;
             Q43648
Q43648;
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                                                                                                                                                                     81 NKRTQPTFGFTVNWKFSESTTVFTGCFTDRNCKEVLKTWWLLRSSVNDIGDDWKATRVG 140
                                                                                                                                                      90 NKRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beuning L.L., Springs T.W., Christeller J.T.,
"Evolution of the proteinase inhibitor I family and apparent lack of hypervariability in the proteinase contact loop.";
J. Mol. Evol. 39:644-654(1994).
EMBL: X67550; CAA48136.1;
EMBL: X67675; CAA44307.1;
HSSP; P19873; 1HVM.
                                                                                                                      1 PGLSARKCSLTGKWDNDLGSNMTIGAVNSKGEFTGTYTTAVTATSNEIKESPLHGTQNTI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                        30 PEIPARKCSLTCKWTNDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ospermatophyta; Spermatophyta; Core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
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                                                           Length 152;
                                                                                  4; Indels
            POTENTIAL,
04B4965B670B974B CRC64;
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                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        strain-cv. ilam HarDr;
MEDLINE=94105328; PubMed=8278532;
Bening L.L. Christeller J.T.;
Isolation of a cona for proteinase inhibitor I.";
Plant Physiol, 102:1061-1061(1993).
                                                         Score 670; DB 13;
Pred. No. 3.2e-57;
; Mismatches 4;
                                                                                                                                                                                                                                                                                         107 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD002604; Potato_inhibit; 1. PROSITE; PS00285; POTATO_INHIBITOR: 1. Serine protease inhibitor. seguence 107 Aa; 12148 MW: DARGGERE
                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000864; Potato_inhibit, Pfam: PF00280; potato_inhibit; 1. PRINTS; PR00292; POTATOINHERR.
                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=95106304; PubMed=7807552;
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            24 Po
16742 MW;
                                                           79.3%;
95.5%;
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                                                                                                                                                                                                                                                                                                                                                                      Solanum tuberosum (Potato).
                                                                                   Conservative
                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 PROTEINASE INHIBITOR I,
                                                                                                                                                                                                      150 INIFTRLRIQKE 161
                                                                                                                                                                                                                     AA;
                                                                      Similarity
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SEQUENCE FROM N.A.
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                       152
                                                          Query Match
Best Local Simi
Matches 126;
                       SEQUENCE
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 Signal.
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RESULT

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Gaps
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STRAIN-CV. ILAM HARDY: TISSUE-POTATO TUBER;
MEDLINE-95106304; Pubmed-7807552;
MEDLINE-95106304; Pubmed-7807552;
MEDLING J.L., Springs T.W., Christeller J.T.;
"Evolution of the proteinase inhibitor I family and apparent lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apparent lack of
                                                                                                                              Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; Asteridae, euasterids I; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodom; PD002604; Potato_inhibit; 1.
PROSITE; PS00285; POTATO_INHIBITOR; 1.
SEQUENCE 107 Aa; 12178 MW; DAADCDB3F11D8811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 AA; 12075 MW; 0CB4A72602D2B4E2 CRC64;
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SEQUENCE FROM N.A.
STRAIN-CV. ILAM HARDY, TISSUE-TUBER,
STRAIN-CJ. Pubmed-7807552;
Beuning L.L., Spriggs T.W., Christeller J.T.;
"Evolution of the proteinase inhibitor I family and
                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-NOV-1996 (TrEMBLrel. 01, Created)
1-NOV-1996 (TrEMBLrel. 01, Last Sequence update)
1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                               hypervariability in the proteinase contact loop."; ", "MOL, EVOL, 39:644-654(1934).
EMBL: LOG137, AAA69780.1; --
HSSP, P19879; 1HFW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypervariability in the proteinase contact loop.";
J. Mol. Evol. 39:644-654(1994).
EMBL; L06985; AAA72133.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.9%; Score 151; DB 10; 93.8%; Pred. No. 3.2e-07;
107 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR000864; Potato_inhibit. Dfam; DF00280; potato_inhibit; 1. PRINTS; PR00292; POTATOINHBTR.
                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00292; POTATOINHBIR.
                                                         01-NOV-1996 (TrEMBLrel, 01, 01-DEC-2001 (TrEMBLrel, 19, PROTEINASE INHIBITOR I.
                                       01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 93.8
Matches 30; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                       01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P19873; 1HYM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-4113;
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SEQUENCE
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SEQUENCE
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        DDT REAL POLICE OF COLORS 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bisgrove B.W.; "Evolution of the fibropellin gene family and pattern of fibropellin gene expression in sea urchin phylogeny."; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases. EMBL: L33861; AAA29955.1; -- HSSP; POB709; 1BF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 FGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVGINIFTR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heliocidaris erythrogramma (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
                                                            0
     Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 16.1%; Score 136; DB 5; Length 529; Best Local Similarity 34.5%; Pred. No. 6.4e-05; Matches 41; Conservative 16; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00022; EGF_1; UNKNOWN_11.
PROSITE; PS01186; EGF_C3; 10.
PROSITE; PS01187; EGF_C4; 7.
Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529 AA; 55543 MW; D4AE958FCF9ACB5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Score 146; DB 10;
Pred. No. 9.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000168; Avidin.
InterPro; IPR000686; Avidin.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR001438; EGF_G2.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EdF_II.
InterPro; IPR001438; EdF_II.
InterPro; IPR001438; EdF_II.
InterPro; IPR001438; EdF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR00149; EGF_II.
InterPro; IPR0011; II.
INTERPRO; IPR0011; IPR0011; II.
INTERPRO; IPR0011; IPR0
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                                                                                                                                                                                                                                                                                                                   529 AA
                                                            1; Mismatches
                                                                                                              2 ESKFAHIIVFFLLATPFETLLARKESDGPEI 32
                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                   PRT;
17.3%;
93.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBROPELLIN IA (FRAGMENT).
                                                            Conservative
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                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                       Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heliocidaris.
NCBI_TaxID=7634;
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SEQUENCE
     Query Match
                                                                                                                                                                                                                                                                                                             Q25058
Q25058;
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Q25058
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Q25059
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332 HYEFPSFGFTVVRDNGRSTTSWTGQCHLCA-GQEVLYTTWIESNWVDTCEDIKKANKVGQ 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 RTQ-PTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVGI 150
                                                                                                                                                                                                                                                                                            Bigrove B.W.; "Evolution of the fibropellin gene family and pattern of fibropellin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 CSLTGKWTNDLGSNMT1GAVNSRGEFTGTY1TAVTATSNEIKESPL-HGTQNTI----NK 91
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
WOUND-INDUCIBLE PROTEINASE INHIBITOR I (FRAGMENT).
Solanum tubersoum (Potato).
Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
| [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metažoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                   gene expression in sea urchin pylogeny,";
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
HSSP, P00740; LDBM.
Interpro; IPR000152; Asx hydroxyl.
Interpro; IPR000088; Avidin.
Interpro; IPR000154; Asx hydroxyl.
Interpro; IPR000156; EGF_2.
Interpro; IPR000188; EGF_11ke.
Interpro; IPR000188; EGF_II.
Interpro; IPR000188; EGF_II.
Interpro; IPR000188; fibronectin_type_1.
Interpro; IPR000083; fibronectin_type_1.
Interpro; IPR002049; Laminin_EGF.
IPR001881; Avidin; I.
IPR001881; Avidin; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01186; EGF_2; 6.
PROSITE; PS01187; EGF_CA; 5.
Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43475 MW; EC89CCE8ABB7E89A CRC64;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FIBROPELIN III (FRAGMENI).
Heliocidaris erythrogramma (Sea urchin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO0011; EGFLAMININ.
PRINTS; PRO0012; FNTYPEI.
SMART; SM00179; EGF_CA; 7.
SMART; SM00019; EGF_CA; 7.
SMART; SM0001; EGF_LA,
PROSITE; PS00010; ASX_HYDROXL; UNKNOWN_7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF_1; UNKNOWN_7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                              Heliocidaris.
NCBI_TaxID=7634;
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DKWTR 395
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Marchantiales; Marchantiaceae; Marchantia.
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Best Local Similarity
                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Q9VQY1;
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                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
SEQUENCE FROM N.A.
STRAIN-KESZTHELYI 855 (WHITTE LADY); TISSUE-ETIOLATED SHOOT;
MEDLINE-96198594; Pubmed-892888;
MEDLINE-96198594; Pubmed-892888;
Manfalvi I., Molndr A., Molndr G., Idkatos L., Szabo L.;
Starch synthesis, and tuber storage protein genes are differently expressed in solanum tuberosum and in Solanum brevidens.",
FEBS Lett. 383:159-164(1996).
FEBS Lett. 383:159-164(1996).
HSSP; P19873; LHXM.
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. RUSSET BURBANK;
Led J.S., Yang Y.S.;
"Nuclootide sequence of 5' flanking region of potato proteinase inhibitor I gene.";
Submitted (UUL-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; Z14027; CA78402.1; -.
NON_TER 30
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                                                                                                                                                                                                      Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%; Score 97; DB 10; Length 30; 76.9%; Pred. No. 0.011; cive 2; Mismatches 4; Indels
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                     101 AA; 11396 MW; A27E65CADE4D1CFA CRC64;
                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEINASE INHIBITOR I (FRAGMENT),
solanum tuberosum (Potato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 AA; 3439 MW; 6090AB9BDA387D40 CRC64;
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                                                                                                                                                                                                      Query Match
Best Local Similarity 92.3%; Pred. No. 0.00019;
Matches 24; Conservative 1; Mismatches 1;
                                                                                                                                   ProDom; PD002604; Potato_inhibit; 1.
PROSITE; PS00285; POTATO_INHIBITOR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                               30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1395 AA
                                                                                                   InterPro; IPR000864; Potato_inhibit, Dfam; PP00280; potato_inhibit; 1. PRINTS; PR00292; POTATOINHETR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marchantia polymorpha (Liverwort).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (Tremblrel. 01, 01-NOV-1996 (Tremblrel. 01, 01-DEC-2001 (Tremblrel, 19, TRNA-GLY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4113;
                                                                                                                                                                       SEQUENCE
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-!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE. AND CF(0) - THE MEMBRANE PROTON CHANNEL. (CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETAA(1), DELTA(1), EDSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE APPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSTER: PSOGO78; rvt; 1. PREFEATS_1; UNKNOWN_1. PROSTER: PSOGO78; WD-binding; CF(1); Hydrogen ion transport; Hydrolase; ATP-binding; CF(1); Hydrogen ion transport; Hydrolase; Mitochondrion; RNA-directed DNA polymerase. SEQUENCE 1395 AA: 156997 MW; 33DD91CF184F9686 CRC64;
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MEDLINE-22114051; PubMed-1731062; Odd K., Takemura M., Nozato N., Odd K., Tamato K., Ohta E., Nakamura Y., Takemura M., Nozato N., Kohchi T., Ohyama K.; Rohchi T., Ohyama K.; Gene organization deduced from the complete sequence of liverwort matching polymorpha mitochondrial genome. "1992).

Michanial genome. "1992).
                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Takemura M., oda K., Yamato K., Ohta E., Nakamura Y., Nozato N.,
Akashi K., Ohyama K.;
Reene clusters for ribosomal proteins in the mitochondrial genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92350681:
MEDLINE-92350681:
MEDLINE-92350681:
Oda K., Vanmato K., Ohta E., Nakamura Y., Takemura M., Nozdto N.,
AKGShi K., Ohyama K.;
"Transfer RNA genes in the mitochondrial genome from a liverwore,
Marchantia polymorpha: the absonce of chloroplast-like tRNAS.";
Nucleic Acida Res. 20:3773-3777(1992).
-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 VFFLLATPFETLLARKESDG----PEIPARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; Length 1395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      liverwort, Marchantia polymorpha.";
Nucleic Acids Res. 20:3199-3205(1992).
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Pfam; PF02874; ATP-synt_ab_N; 1.
Pfam; PF01348; Intron_maturas2; 1.
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RA Adams M.D., Celniker S.E., Lip P.W., Hoskins R.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.E., Strichards S. Ashburner M. Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Radron R.C., Rogers Y.-H.C., Blazej R.G., Champpe M., Pfeiffer B.D., RA Man K.H., Doyle C. Barter E.G., Helt G., Champpe M., Pfeiffer B.D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfeinorkoch C., Baldwin D., Ballew R.M., Basu A., Barondale J., Bayraktrorglu L., Beasley E.M., Baltis R.C., Busam D.A., Burtler H., Caddeu E., Center A., Chandra I., RADROVAO E.D., Botchan M.R., Bouck J., Bayckstein P., Botchare P., Chandra I., RADROVAO E.D., Botchan M.R., Dong C., Mays A.D., Dew I. Dietz S.M., Cawley S., Dahlke C., Davamon M.R., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Roder C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., R. Houton K.A., Howland T.J., Weil M.-H., Ibegwam C., Jalall M., Kalush F., Karpen G.H., Ke.Z., Kennison J.A., Ketchum K.A., Jalall M., Kalush F., Karpen G.H., Ke.Z., Kennison J.A., Ketchum S.M., Mattei B., McIntosh T.J., Weil M.-H., Durik C.J., Lisng Y., Lin X., Mattei B., McIntosh T.C., Moredod M.P., McPherson D., McRond M.B., McCheod M.P., McPherson D., McRond M.B., McIntosh K.J., Mattei B., McIntosh K.J., Murphy L., Muzny D.M., Norther S., Shen H., Shie B.C., Siden-Kiamos I., Simpson M., Strong R., Sin S., Shen H., Shie B.C., Siden-Kiamos I., Simpson M., Strong R., Sin R., Woodage T., Stapheton M., Strong R., Sin S., Shen H., Shie Shie B.C., Siden-Kiamos I., Simpson M., Strong S., Yao, Q.A., Wallen S.W., Woodage T., Shon M., Yang S., Yao, Q.A., Wallen S., Wallen S.W., Woodage T., Shon M., Yang S., Yao, Q.A., Wallen S., Wassarman D.A., Weinstock G. W., Weissenbach J.C., Scheeler E., Spradling M.C., Stapheton M., Yang S., Zhu X., Shien F., Scheeler S., Stapheton M., Yang S., Zhu X., Shien F., Scheeler S., Stank S
                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin domain; Repeat.
SEQUENCE 400 AA; 44386 MW; EEF5841C1B406DF6 CRC64;
  Created)
Last sequence update)
Last annotation update)
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InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003961; FN_III.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MKC.
Pfam; PF00041; fin3; 1.
                                                                                                     Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                      MEDLINE-20196006; PubMed-10731132;
  13,
16,
19,
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01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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SMART; SM00060; FN3; 1
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                             CG15427 PROTEIN.
CG15427.
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Gaps

53;

10.0%; Score 84.5; DB 5; Length 400; 26.6%; Pred. No. 4.4; ive 17; Mismatches 54; Indels 53

Best Local Similarity 26.6 Matches 45; Conservative

Query Match

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54 GAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTINKRTQPTFGFTVNWKFSESTTVFT 113
                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597 TIENLRREDFGYYQCVV---SNEV--ATLMAVTQLVIEGTQPHAPYNITGKATESS--IT 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                   173 ETLYQRKVGDSVEMHCDALEAEGTERP-----TIKWQRQEGEQLTESQRNRIKISGGNI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 ETLYQRKVGDSVEMHCDALEAEGTERP-----TIKWQRQEGEQLTESQRNRIKISGGNI 596
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J. Neurosci. 21:3113-3125(2001).
BMEL, AJ312133; CAC39162.1; -... NON_TER 749
749
SEQUENCE 749 AA: 83346 MW; B6B365C3D4C313E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 749;
                                                                                                                                             114 GQCFIDRNGKEVLK---TMWLLRSSVNDIGDDWK-----ATRVGIN 151
                                                                                                                                                                     280 LQWLPGYSGGSEYKQDYTIWFREAGVN----DWQTISVTPSGSTQVTIN 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650 LQWLPGYSGGSEYKQDYTIWFREAGVN----DWQTISVTPSGSTQVTIN 694
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   ---ESDGPEIPARKCSLTGKWTNDLGSNMT-
                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
TURTLE PROTEIN, ISOFORM 2 (FRAGMENT).
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Last annotation update)
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Pred. No. 9.3;
                                                                                                                                                                                                                                                                            749 AA
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26.6%;
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Best Local Similarity
Matches 45; Conserv
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 ETLLARK--
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update) DNA POLYMERASE III-LIKE PROTEIN, GAMMA SUBUNIT.
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01-OCT-2000 (
01-DEC-2001 (
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
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Bodily K.D., Morrison C.M., Renden R.B., Broadie K., A. Novel Member of the 19 Superfamily, turtle, is a cns-specific ProfeinRequired for Coordinated Motor Control."; J. Neurosci. 21:3113-3125(2001).
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BEGUENCE FROM N.A.

MEDLINE-21212253; PubMed-11312296;

BOdliy K.D., Moritson C.M., Renden R.B., Broadle K.;

BOdliy K.D., Moritson C.M., Renden R.B., Broadle K.;

Novel Member of the Ig Superfamily, turtle, is a CNS-Specific ProteinRequired for Coordinated Motor Control.";
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Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
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                                                                                                                                                                                                                                 54; Indels
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EMBL: AJ312135; CAC39164.1;
SEQUENCE 1531 AA; 171015 WW; CDADDB21EC53C33A CRC64;
                                                                      J. Neurosci. 21:3113-3125(2001).
EMBL; AJ312134; CAC39163.1; -.
SEQUENCE 903 AA; 100467 MW; F7D055B4AFDE4ELD CRC64;
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                                                                                                                                                                                     Score 84.5; DB Pred. No. 12; 7; Mismatches
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17; Mismatches
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26.6%;
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01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
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Matches 45; Conservative ]
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Best Local Similarity 26.6'
Matches 45; Conservative
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STRAINECY. COLUMBIA, when we have a second of the property of 
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STRAIN-CV. COLUMBIA,
MARKS M.D., Prigge M., Shi H.;
MATCS M.D., Prigge M., Shi H.;
MATCS M.D., Prigge M., Shi H.;
MATCS M.D., Prigge M., Shi H.;
Super Stabidopsis STI gene is a member of the replication factor C-like gene family."
Submitted (MAX-2000) to the EMBL/Genbank/DDBJ databases.
EMBL, AF264023; AAF82285.1: -.
Arabidopsis thallana (Mouse-ear cress).

Bukaryophyta; Uridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
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STI.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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INTELPIC; IPR003959; AAA_SUbfam.
InterPro; IPR000862; RFC.
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Best Local Similarity 24.89
Matches 30; Conservative
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STRAIN-CV. COLUMBIA;
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DR InterPro; IPR003959; AAA_subfam.

DR InterPro; IPR000862; RFC.

DR Pfam; PF00004; AAA; 1.

Query Match

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September 17, 2002, 15:41:34 ; Search time 11.91 Seconds (without alignments) 523.413 Million cell updates/sec
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845
1 MESKFAHIIVFFLLATPFET......DWKATRVGINIFTRLRTQKE 161
GenCore version 4.5
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                                                                         OM protein - protein search, using sw model
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

105224

Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Searched:

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	01 gallus	34 gallus	33 gallus	36 gallus	53 gallus	35 gallus		solanum		P05118 lycopersico									P40426 homo sapien	_	P50401 cellulomona	013359 candida alb	Q44602 buchnera ap			Q02496 mus musculu	_		•	_	P09298 varicella-z	bos tauru	Q03947 shigella dy
SUMMARIES	QI	>	AVR4_CHICK	AVR3_CHICK	AVR7_CHICK	AVR1_CHICK	AVR6_CHICK	AVR2_CHICK	ICID_SOLTU	ICI1_SOLTU	ICI1_LYCES	SAV1_STRVL	SAV_STRAV	FBP1_STRPU	SAV2_STRVL	ICI1_LYCPE	FBP3_STRPU	UGDH_CAEEL	EFG_MICLU	PBX3_HUMAN	PGCN_MOUSE	GUXA_CELFI	KEX2_CANAL	TRPD_BUCSC	PBX1_HUMAN	PET2_HUMAN	MUC1_MOUSE	FIBP_ADECT	CDG2_PAEMA	RPOD_GUITH	MURE_BUCAP	VGLM_VZVD		IPAD_SHIDY
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фP	Query Match	80.	59.1	55.5	55.3	54.2	54.1	52.5	18.2	16.9	16.9	16.9	16.9	16.6	16.5	16.1	14.7	10.1	9.5	9.5	8.8	8.8	8.7	8.2	8.5		8.3	8.5	8.5	8.2	8.		8.1	8.0
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	Result No.	П	7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P25927 salmonella P32171 escherichia	P18159 bacillus su P22316 cyprinus ca	P05787 homo sapien P10486 escherichia	P06838 saccharomyc	O15165 homo sapien O04658 saccharomyc	P32506 cercopithec	P30999 mus musculu	P48979 prunus pers
BIGA_SALTY RHAB_ECOLI	YHXB_BACSU CCAS_CYPCA	K2C8_HUMAN T1R1_ECOLI	RA10_YEAST	C181_HUMAN	PVR_CERAE	CTD1_MOUSE	PGLR_PRUPE
			Η.		П	П	٦
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8 8 0 0 8	8 8 0.0	0.7 0.6	7.9	6.7	7.8	7.8	7.8
68 67.5	67.5 67.5	67	66.5	66.5 66	99	99	65.5
34 35	36 37	8 6 8 8	40	4 7	43	44	45

ALIGNMENTS

SULT 1 ID_CHICK	ID AVID_CHICK STANDARD; PRT; 152 AA. AC PO2701: 091958:	21-JUL-1986 (Rel. 01, Creat 01, Nov-1991 (Rel. 20, Last 16, Oct. 20, University 16, Oct. 20,	Avidin precursor. AVD.	Gallus gallus (Chicken).		OC Gallus. OX NCBI_TaxID=9031;		SEQUENCE FROM N.A. MEDLINE=87203384; PubMed=3575102;	RA Gope M.L., Keinaenen R.A., Kristo P.A., Conneely O.M., Beatie W.G., RA Zarucki-Schulz T. O'Malley R W. Kulomaa M S.	RT "Molecular cloning of the chicken avidin cDNA.";	RL Nucleic Acids Res. 15:3595-3606(1987). RN [2]		RX MEDLINE=90355928; PubMed=2143802;	"Cloning and		KN [3] RP SECITENCE FROM N.A.		RX MEDLINE=95394357; PubMed=7665080; PA Mallon M. I Tankbanon M.O. Kulomaa M.S.		and its relationship with the avidin-related genes Avrl-Avr5.";	RL Gene 161:205-209(1995). RN [4]		RX MEDLINE=71107558; PubMed=5100763;	"Egg white avidin. 3. Sequence of the 78-residue	bromide peptide. Complete amino acid sequence of the pro			RP IMPORTANCE OF TYR IN BIOTIN-BINDING. RX MEDI, INE=90351377: PubMed=2386489:	Gitlin G., Bayer E.A., Wilchek M.;	RT "Studies on the biotin-binding sites of avidin and streptavidin.	Biochem. J. 269:527-530(1990).			RA Hiller Y., Bayer E.A., Wilchek M.;	RI "Studies on the Diotin-Dinaing site of Aviain, Minimized Ifagments RT that bind biotin,";	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY; SYNTHESIZED IN HEN OVIDUCT AND CONCENTRATED IN EGG WHITE (WHERE IT REPRESENT 0.05% OF THE TOTAL PROTEIN).
                                                                                                                                                                                                                                                                                                                                  Nardone E., Rosano C., Santambrogio P., Curnis F., Corti A., Magni F., Sicardi A., Arosio P., Pagnelli G., Losso R., Apreda B., Bolognesi M., Sidoli A., Arosio P.; Bolognesi M., Blochemical characterization and crystal structure of a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                      BIOTIN (NON-COVALENT).

I -> T (IN APPROX, 50% OF THE CHAINS).

G -> S (IN REF. 3).

E -> Q (IN REF. 2 AND 3).
                                                                                                                                                                                 Pugliese L., Coda A., Malcovati M., Bolognesi M.;
"Three-dimensional structure of the tetragonal crystal form of
egg-white avidin in its functional complex with biotin at 2.7-A
resolution.";
                                                                 Livnah O., Bayer B.A., Wilchek M., Sussman J.L.; "Three-dimensional structures of avidin and the avidin-biotin
                                                                                                                     roc. Natl. Acad. Sci. U.S.A. 90:5076-5080(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Signal; Biotin; 3D-structure. SIGNAL
                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
MEDLINE-93294833; Pubmed=8515446;
                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE-98430987; Pubmed-9760187;
                             K-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                 MEDLINE-93281699; PubMed-8506353;
                                                                                                                                                                                                                                                       J. Mol. Biol: 231:698-710(1993).
Biochem. J. 278:573-585(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X05343; CAA28954.1; -. EMBL; L27818; AAB59733.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB; ZCAM; 15-JUL-98.
InterPro; IPR000088; Avidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00709; AVIDIN.
ProDom; PD016055; Avidin; 1.
PROSITE; PS00577; AVIDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01382; Avidin; 1.
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PIR; S11540; S11540.
PDB; ZAVI; 15-UUL-93.
PDB; 1AVD; 31-UAN-94.
PDB; 1AVY; 15-JUL-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A03160; VICH.
PIR; A27518; A27518.
PIR; S11540; S11540.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 NKRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMMLLRSSVNDIGDDWKATRVG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                  1 DCLSARKCSLTCKWTNDLGSNWT1GAVNSRGEFTGTYITAVTATSNEIKESPLHGTENTI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O.,
Toimela T.A., Helenius M.A., Kulomaa M.S.;
"Molecular cloning and nucleotide sequence of chicken avidin-related
genes 1-5.";
                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                          30 PEIPARKCSLIGKWINDLGSNMTIGAVNSRGEFIGTYITAVTATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur. J. Biochem. 220:615-621(1994).
-!- MISCELLANEOUS: THE SEQUENCES OF THE CODING REGIONS OF GENES AVRA
AND AVRS ARE IDENTICAL.
                                                                                                                                                                                                                                                                                Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY; BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
                                                                                                                                                                                                                                                      1D55A4491D5EFD5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Avidin-related protein 4/5 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-WHITE LEGHORN; TISSUE-Oviduct; MEDLINE-94170814; PubMed-8125122:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000088; Avidin.
Pfam: PF01382; Avidin; 1.
PRINTS; PR00709; AVIDIN.
ProDom: PD016055; Avidin; 1.
PROSITE: PS00577; AVIDIN; FALSE_NEG.
Biotin; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z22883; -; NOT_ANNOTATED_CDS, HSSP; P02701; 1RAV.
58
77
77
84
109
1124
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16769 MW;
                                                                                                                                                                                                                                                                                                                                Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Gallus gallus (chicken).
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152 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
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ID AVR4_CHICK
                                                                                                                                                                                       STRAND
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                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                 90 NKRTQPIFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=WHITE LEGHORN; TISSUE-Oviduct; MEDIATE-170814; PubMed-8125122; REIATE-94170814; PubMed-8125122; Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O., Toimela T.A., Helenius M.A., Kulomaa M.S.; "Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5."; Eur. J. Biochem. 220:615-621(1994).
                                                                                                                                                                                                                    AVIDIN-RELATED PROTEIN 4/5.
BIOTIN (NON-COVALENT) (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
946C6C6310EFE13A CRC64;
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BIOTIN (NON-COVALENT) (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
84DC03926A6BE2IC CRC64;
                                                                                                                                                                                                  30 PEIPARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI
                                                                                                                                 59.1%; Score 499; DB 1; Length 150; 75.0%; Pred. No. 7.2e-43; ive 8; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Avidin-related protein 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biotin; Signal; Multigene family, SIGNAL 1 24 POTENTIAL. CHAIN 25 150 AVIDIN-RELL. BINDING 57 57 BIOTIN (NO) 2ARBOHYD 93 93 N-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 221612; -; NOT_ANNOTATED_CDS.
EMBL; 221536; -; NOT_ANNOTATED_CDS.
HSSP; P02701; IRAV.
InterPro; IPRO00088; Avidin.
150 AV
57 B1
67 N-
93 N-
141 N-
16644 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01382; Avidin; 1.
PRINTS; PR00709; AVIDIN.
ProDom; PD016055; Avidin; 1.
PROSITE; PS00577; AVIDIN; 1.
                                                                                                                                                                   99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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139 YNNFTRLCTVEE 150
                                                                                                                                                                                                                                                                                                                                 150 INIFTRLRTQKE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 1
150 AA;
                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVR3_CHICK
P56733;
                                                                                                                                 Query Match
Best Local S
Matches 99
                                                                CARBOHYD
SEQUENCE
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                                               CARBOHYD
 CHAIN
BINDING
                                  CARBOHYD
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                                 ä
                                                                                                                           90 NKRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                               30 PEIPARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization and chromosomal localization of the chicken avidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-RHODE ISLAND;
Ahlroth M.K., Kola E.H., Ewald D., Masabanda J., Sazanov A., Fries
Kulomaa M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.

BOTHLAREATED PROTEIN 7.

BIOTIN (NON-COVALENT) (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

MAY 30F335611F65923D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
55.5%; Score 469; DB 1; Length 150; 69.7%; Pred. No. 7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene family.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.3%; Score 467; DB 1; 68.9%; Pred. No. 1.1e-39;
                                                                                                                                                                                                                                                                                        CHICK STANK-
AVR7_CHICK STANK-
P56736; Q9W6V4;
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last annotation update)
                               11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ237659; CAB39894.1; HSSP; PO2701; 1RAV. InferPro; IPRO000088; Avidin. Pfar. PP01389; Avidin. 1. PRINTS; PR00709; Avidin; 1. ProDom; PD016055; Avidin; 1. PROSITE; PS00577; AVIDIN; 1. PROSITE; PS00577; AVIDIN; 1. 24 SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16543 MW;
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91; Conservative
                                                                                                                                                                                                              | ||| || :|
139 YNNFTRORTVEE 150
                                                                                                                                                                                          150 INIFTRLRTQKE 161
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              Similarity
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                               92;
 Query Match
Best Local S
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CARBOHYD
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CARBOHYD
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Best Local
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Best Local Similarity
Matches 89: Conserv
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                                                                                         90 NKRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                                                      79 KRACOPTEGETVHWNFSESTSVEVGOCFIDRSGKEVLKTKWLORLAVDDISDDWKATRVG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
30 PEIPARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI 89
                        21 PGLSARKCSLTGEWDNNLGSNWTIGAYNDNGEFNGTXITAYADNPGNIKLSFLLGIQH-- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O.,
Toimela T.A., Helenius M.A., Kulomaa M.S.;
"Molecular cloning and nucleotide sequence of chicken avidin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVIDIN-RELATED PROTEIN 1.
BIOTIN (NON-COVALENT) (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
77548380B995B1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes for chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes 1-5.";
Eur. J. Biochem. 220:615-621(1994).
-1- SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keinaenen R.A., Laukkanen M.-L., Kulomaa M.S.; "Molecular cloning of three structurally related
                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
30-MAY-2000 (Rel. 39, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO00088; Avidin.
Pfam; PF01382; Avidin; 1.
PRONTS; PR00709; AVIDIN.
ProDom; PD016055; Avidin; 1.
PROSITE; PS00577; AVIDIN; 1.
Biotin; Signal; Multigene family.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=WHITE LEGHORN; TISSUE=Oviduct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 221611; -; NOT_ANNOTATED_CDS.
EMBL; 297063; CAB09798.1; -.
HSSP; P02701; 1RAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Avidin-related protein 1 precursor.

    Steroid Biochem. 30:17-21(1988).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Oviduct;
MEDLINE-88260103; PubMed~2838690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94170814; PubMed-8125122;
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93
16468 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
                                                                                                                                                                                                                  139 YNNFTRORTVEE 150
                                                                                                                                                                                        150 INIFTRERTQKE 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                     AVR1_CHICK
013153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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BINDING
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DB 1; Length 150;

54.2%; Score 458;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEĞÜENCE FROM N.A.
STRAXIN-RHODE ISLAND;
Ahlroth M.K., Kola E.H., Ewald D., Masabanda J., Sazanov A., Fries R.,
Kulomaa M.S.;
                                                                                                                                                                       90 NKPTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                    83
                                                                                                       Gaps
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization and chromosomal localization of the chicken avidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 PEIPARKCSLTGKWTNDLGSNWTIGAVNSRGEFTGTVITAVTATSNEIKESPLHCTONTI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOTIN (NON-COVALENT) (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
COF3357D6291B150 CRC64;
                                                                                PEIPARKCSLTGKWTNDLGSNWTIGAVNSRGEFTGTXITAVTATSNEIKESPLHGTQNTI
                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
           8.8e-39;
ches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biotin; Signal; Multigene family.
SIGNAL 1 24 POTENTIAL.
CHAIN 25 150 AVIDIN-RELATED PROTEIN 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                Pred. No. 8.86
L: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Avidin-related protein 6 precursor
67.48; Pic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ237658; CAB39893.1; -. HSSP; PO2701; IRAV.
InterPro: IPR000088; Avidin. Pfam; PF001382; Avidin; 1. PRINTS; PR00709; AVIDIN. ProDom; PD016055; Avidin; 1. PROSITE; PS00577; AVIDIN; 1.
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54 54 N-
93 N-
141 141 N-
150 AA; 16528 MW;
                                         Conservative
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139 NNDFTRORTVEE 150
                                                                                                                                                                                                                                                              150 INIFTRLRTQKE 161
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene family.
Submitted (M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 68
                                                                                                                                                                                                                                                                                                                                                                                                                      AVR6_CHICK
P56735;
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AA.

107

STANDARD;

08, Created)

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139 NNDFTROHTVEE 150
                                                                              01-AUG-1988 (Rel.
                                                       ICID_SOLTU
P08454;
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CONFLICT
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                                              ICID_SOLTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                   RESULT
                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
90 NKRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVG 149
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 NKRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                                                                                                                                                                                                                                     Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O.,
Toimela T.A., Helenius M.A., Kulomaa M.S.;
"Molecular cloning and nucleotide sequence of chicken avidin-related
genes 1-5.";
Eur. J. Biochem. 220:615-621(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVIDIN-RELATED PROTEIN 2.
BIOTIN (NON-COVALENT) (BY SIMILARITY).
B-LIKKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 PEIPARKCSLTGKWTNDLGSNWTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.5%; Score 444; DB 1; Length 150; 65.9%; Pred. No. 2.2e-37; ive 12; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                              -! - SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     763D1E2B1A93A66D CRC64;
                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Avidin-related protein 2 precursor.
                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biotin; Signal; Multigene family.
SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-WHITE LEGHORN; TISSUE-Oviduct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD016055; Avidin; 1.
PROSITE; PS00577; AVIDIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z21554; -; NOT_ANNOTATED_CDS.
EMBL; Z21535; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                            MEDLINE-94170814; PubMed-8125122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 N
16434 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000088; Avidin.
Pfam; PF01382; Avidin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87; Conservative
                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00709; AVIDIN.
                                                                                                                                                                                                    Gallus gallus (Chicken).
                                                        | ||| || :|
139 YNNFTRORTVEE 150
                                           150 INIFTRLRTQKE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 INIFTRLRTQKE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P02701; 1RAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                         AVR2_CHICK
P56732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                             AVR2_CHICK
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Cleveland T.E., Thornburg R.W., Ryan C.A.; Cleveland T.E., Thornburg R.W., Ryan C.A.; Molecular characterization of a wound-inducible inhibitor I gene from potato and the processing of its mRNA and protein."; Plant Mol. Biol. 8:199-207(1987).
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Wound-induced proteinase inhibitor I precursor (Chymotrypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richardson M., Cossins L.;
FEBS Lett. 52:161-161(1975).

-!- FEBN Lett. 52:161-161(1975).

-!- FUNCTION: INHIBITS BOTH CHYMOTRYPSIN AND TRYPSIN.

-!- SUBUNIT: HETEROGENEOUS TETRAMERS OF SIMILAR CHAINS.

-!- SUBUNIT: HETEROGENEOUS TETRAMERS OF SIMILAR CHAINS.

-!- SUBUNIT: HETEROGENEOUS TETRAMERS OF SIMILAR CHAINS.

-!- SUBUNIT: HETEROGENEOUS TETRAMERS OF A FACTOR FROM THE WOUND SITE. WITHIN THE LEAVES IT INDUCES THE CYTOPLASMIC SYNTHESIS OF PROTEINARE INHIBITORS I AND II.

-!- SIMILARITY: BELONGS TO THE POOTATO CHYMOTRYPSIN INHIBITOR I FAMILY OF SERINE PROTEASE INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Richardson M., Cossins L.; "Chymotryptic inhibitor I from potatoes: the amino acid sequences of subunits B, C, and D."; FEBS Lett. 45:11-13(1974).
                                                                                                    I, D subunit).
Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WOUND-INDUCED PROTEINASE INHIBITOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 154; DB 1; Length 107; Pred. No. 1.2e-08;
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-> S (IN REF. 1).
3964CF60D81D2349 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF 37-107 (SUBUNITS B; C AND D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probom; P0002604; Potato_inhibit; 1.
PROSITE; PS00285; POTATO_INHIBITOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P19873; 1HYM.
Interpro; IPR000864; Potato_inhibit.
Pfam: PF00280; potato_inhibit; 1.
PRINYS; PR00292; POTATOINHETR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease inhibitor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 37-107 (SUBUNITS B; C
STRAIN-CV. ULSTER PRINCE;
MEDLINE-75008020; PubMed-4606338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ψ.
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us-09-743-690-7.rsp

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Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081, 4082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of tomato."
                                                                                                                                                                                                                                                                                                                                                    Ryan C.A.
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SEQUENCE
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CHAIN
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      Gaps
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                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Proteinase inhibitor i precursor.
Solanum tuberosum (Potato).
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum (Tomato), and Lycopersicon pervianum (Pervian Comato).
Lycopersicon pervianum (Pervian Comato).
Eukaryora, Viridiplantae: Streptophyta; Eukaryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudioctyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain-cv. russer burbank;
Lee J.S., Park J.S.;
Nucleotide sequence of a protease inhibitor I gene in potato.";
korean J. Bot. 32:67-78(1989)..
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                                                                                                                                                                                                                                                                                                                                                                      Spermātophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID-4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REACTIVE BOND (BY SIMILARITY). 52F39C3C913CC052 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.9%; Score 143; DB 1; Length 107; 87.5%; Pred. No. 1.5e-07;
                                              1 MESKFAHIIVFFLLATPFETLLARKESDGPEI----PARKCSLTGKWTNDLG
                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
PROTEINASE INHIBITOR I.
    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Wound-induced proteinase inhibitor I precursor.
                                                                                                                                                                                                 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 AA
    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodom; PD002604; Potato_inhibit; 1, PROSITE; PS00285; POTATO_INHIBITOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro: IPR000864; Potato_inhibit. Dfam; DF00280; potato_inhibit; l. PRINTS; PR00292; POTATOINHBTR.
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12063 MW:
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107 AA;
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SEQUENCE FROM N.A.
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ID ICII_SOLTU
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P05118;
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SEQUENCE
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SPECTES-L.peruvianum;
MEDLINE-911705051; Pubmed-2005119;
Wingate V.P.M., Kyan C.A.;
"A novel fruit-expressed trypsin inhibitor I gene from a wild species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE POTATO CHYMOTRYPSIN INHIBITOR I FAMILY OF SERINE PROTEASE INHIBITOR.
SEQUENCE FROM N.A.
SPECIESEL.esculentum;
MEDLINE-87016930; PubMed-3463966;
MEDLINE-87016930; PubMed-3463966;
MEDLINE-87016930; PubMed-3463966;
Medle U.S., Brown W.E., Grinam U.S., Pearce G., Fox E.A., Dreher T.W.,
Ahern K.G., Pearson G.D., Ryan C.A.;
Mollecular characterization and phylogenetic studies of a wound-
inducible proteinase inhibitor I gene in Lycopersicon species.";
Proc. Natl. Acad. Sci. U.S.A. 83:7277-7281(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "wound-induced proteinase inhibitors from tomato leaves. I. The CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 266:5814-5818(1991).
-!- MISCELTANEOUS: MECHANICAL DAMAGE (I.E., INSECT CHEWING) TO THIS PLANT RESULTS IN THE SYSTEMIC RELEASE OF A FACTOR FROM THE WOUND SITE. WITHIN THE LEAYES IT INDUCES THE CYTOPLASMIC SYNTHESIS OF PROPERINASE INHIBITORS I AND II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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REACTIVE BOND (BY SIMILARITY).
124BAC3400E9F0DG CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Graham J.S., Pearce G., Merryweather J., Titani K., Ericsson L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deduced primary structure of pre-inhibitor I and its
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16.9%; Score 143; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.5e-07;
Matches 28; Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MESKFAHIIVFFLLATPFETLLARKESDGPEI 32
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PIR; A24048; A24048.

PIR; A25046; A25046.

PIR; A39547; A39547; A39547; INMM.

Interpro; IPR000864; Potato_inhibit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEGMI, PEOCRAGO POTATO INTELLA IL PRINTS; PRODUZO: POTATOINHER. Probom, PD002604; Potato_inhibit; I. PROSITE; FS00265; POTATO_inhibit; I. Serine protease inhibitor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         post-translational processing.";
J. Biol. Chem. 260:6555-6560(1985)
                                                                                                                                                                                                                                                                                                                                         SPECIES=L.esculentum;
MEDLINE-85207657; PubMed-2987227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AA; 12585 MW;
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bridges
RESULT 12
SAV_STRAV
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                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1263:60-66(1995).
-!- FUNCTION: THE BIOLOGICAL FUNCTION OF STREPTAVIDIN IS NOT KNOWN.
FORMS A STRONG NON-COVALENT SPECIFIC COMPLEX WITH BIOTIN (ONE
MOLECULE OF BIOTIN PER SUBUNIT OF STREPTAVIDIN).
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
                                                                                                                                                                           [1] SEQUENCE FROM N.A.
MEDLINE-95359204; PubMed-7632734;
Bayer E.A., Kullik T., Adar R., Wilchek M.;
"Close similarity among streptavidin-like, biotin-binding proteins from Streptomyces.";
                                                                                                Streptavidin VI precursor (SA VI).

Streptomyces violaceus (Streptomyces venezuelae).

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycesoe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 QVSAAEAGITGTWYNQLGSTFIVTA-GADGALTGTYESAVGNAESRYVLTGRYDSAPATD
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INVOLVED IN BIOTIN BINDING
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INVOLVED IN BIOTIN BINDING
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INVOLVED IN BIOTIN
                                                                     Last sequence update)
Last annotation update)
                           183 AA.
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                           PRT;
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                                                        Created)
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                           STANDARD;
                                                      (Rel. 35, (Rel. 35, 1) (Rel. 35, 1)
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183
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146 STLVGHDTFTKVK 158
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Best Local Similarity
Matches 43; Conserv
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                                                                                                                                                             NCBI_TaxID=1936
                                                                                 01-NOV-1997
                                                    01-NOV-1997
                                                                     01-NOV-1997
                         SAV1_STRVL
Q53532;
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BINDING
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Argarana C.E., Kuntz I.D., Birken S., Axel R., Cantor C.R.; "Molecular cloning and nucleotide sequence of the streptavidin gene.";
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Katz B.A., Cass R.T.;
"In crystals of complexes of streptavidin with peptide ligands
containing the HPQ sequence the pKa of the peptide histidine is less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alon R., Bayer E.A., Wilchek M.; "Streptavidin contains an RYD sequence which mimics the RGD receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural studies of binding site tryptophan mutants in the high-affinity streptavidin-biotin complex.";
                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90351377; PubMed-2386489;
Gitlin G., Bayer E.A., Milchek M.;
Studies on the biotin-binding sites of avidin and streptavidin.
Tyrosine residues are involved in the binding site.";
Biochem. J. 269:527-530(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 40-157.
MEDLINE-97337436; PubMed-9194176;
Freitag S., le Trong I., Klumb L., Stayton P.S., Stenkamp R.E.;
"Structural studies of the streptavidin binding loop.";
Protein Sci. 6:1157-1166(1997).
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bridges between Asp61 and His87 at low pH.";
J. Mol. Biol. 274:776-800(1997).
                                                                                                                                                                                                                                                                                                                                                                   streptavidin. Tryptophan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98300340; PubMed-9636711; Freitag S., le Trong I., Chilkoti A., Klumb L.A., Stayton P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 37-157 OF MUTANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 170:1236-1241(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 37-157
MEDLINE-98070615; PubMed=9405158;
                                                  (Rel. 19, Last sequence update)
(Rel. 40, Last annotation update)
 AA.
                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 25-64.
MEDLINE=86148514; PubMed=3951999;
 183
                                                                                                                                                                                                                                                                                                                                                                                      residues involved in the active site.";
                                                                                                                                                                                                                                                                                                                            MEDLINE-89134083; Pubmed=3223904;
Gitlin G., Bayer E.A., Wilchek M.;
"Studies on the biotin-binding site of
                                                                                                                                                                                                                                                                         Nucleic Acids Res. 14:1871-1882(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             than 3.0.";
J. Biol. Chem. 272:13220-13228(1997).
[8]
                                                                                                                                                                                                                                                                                                             IMPORTANCE OF TRP IN BIOTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANCE OF TYR IN BIOTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90358825; PubMed=2390089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY OF 37-157
                                   01-AUG-1991 (Rel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. J. 256:279-282(1988).
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain of fibronectin.";
                                                                                        Streptavidin precursor.
                                                                                                             Streptomyces avidinii.
                                                                                                                                                               NCBI_TaxID=1895;
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                                                      01-AUG-1991
                                                                       16-0CT-2001
SAV_STRAV
P22629;
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90 NKRIQPIFGFIVNWK----FSESTIVFIGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWK 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 32.3%; Pred. No. 3.2e-07;
Matches 43; Conservative 20; Mismatches 57; Indels 13
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PDB; 212D; 23-SED-98.
PDB; 212E; 16-SEP-98.
PDB; 212G; 16-SEP-98.
PDB; 212G; 16-SEP-98.
PDB; 212G; 16-SEP-98.
PDB; 212I; 16-SEP-98.
PDB; 21ZI; 16-SEP-98.
PDB; 21ZI; 16-SEP-98.
PDB; 21ZX; 16-SEP-98.
PDB; 2RTA; 18-NOV-98.
PDB; 2RTA; 18-NOV-98.
PDB; 2RTC; 18-NOV-98.
PDB; 2RTG; 18-NOV-98.
PDB; 2RTM; 18-NOV-98.

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Probom; Pp016055; Avidin; 1.
PROSITE; PS00577; Avidin; 1.
Signal; Biotin; 3D-structure.
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STLVGHDTFTWVR 158
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SEQUENCE
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Mel. Biol. 279:211-221(1998).
- FUNCTION: THE BIOLOGICAL FUNCTION OF STREPTAVIDIN IS NOT KNOWN. FORMS A STRONG NON-COVALENT SPECIFIC COMPLEX WITH BIOTIN (ONE MOLECULE OF BIOTIN PER SUBUNIT OF STREPTAVIDIN).
                                                         -:- SUBCELLULAR LOCATTON: Secreted.
-:- SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
-:- DATABASE: NAME-ProZyme technical fact sheet.
WWW-THILD://www.prozyme.com/technical/sal0data.html",
                                                                                                                                                                                                                   EMBL; X03591; CAA27265.1; -. PIR; A23513; A23513.
                                                   -! - SUBUNIT: HOMOTETRAMER.
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04-MAR-98.
04-MAR-98.
04-MAR-98.
04-MAR-98.
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01-NOV-94.
15-MAY-97.
15-MAY-97.
03-APR-96.
03-APR-96.
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1SRE;
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ISRH;
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1RST;
1RSU;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: MODERATE LEVELS IN UNFERTILIZED EGGS AND DOURING EARLY CLEADANGE, THEN RAPIDLY INCREASES IN ABUNDANCE BETWEEN LATE MORULA AND MESENCHYME BLASTULA STAGES TO MAXIMAL LEVELS MAINTAINED THROUGH SUBSEQUENT STAGES. EXPRESSED BOTH MATERNALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dev. Biol. 146:89-99(1991).
-!- FUNCTION: FORM THE APICAL LAMINA, A COMPONENT OF THE EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: EXTRACELLULAR. IN VESICLES IN THE CYTOPLASM OF UNPERTILIZED BGGS, THEN TO THE BASE OF THE HYALIN LAYER THROGEHOUT DEVELOPMENT AND FINALLY IN THE APICAL LAMINA IN LATE EMBRYOS AND EARLY LARVAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: 2 ISOFORMS; IA (SHOWN HERE) AND IB; ARE PRODUCED BY ALTERNATIVE SPLICING. THE SMALL FORM (IB) LACKS 8 EGF
                                                                                                                                                                                                                                         Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89196806; PubMed-2784773;
Hunt L.T., Barker W.C.;
"Avidin-like domain in an epidermal growth factor homolog from a sea
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=90112459; PubMed=2514273;
DelgadillorReynoso M.G., Rollo D.R., Hursh D.A., Raff R.A.;
Structural analysis of the uEGF gene in the sea urchin
Structural supplies of the uEGF gene in the sea urchin
strongylocentrotus purpuratus reveals more similarity to vertebrate than to invertebrate genes with EGF-like repeats.";
J. Mol. Evol. 29:314-327(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91285254; PubMed=2060714;
Bisgrove B.W., Andrews M.E., Raff R.A.;
"Fibropellins, products of an EGF repeat-containing gene, form a
unique extracellular matrix structure that surrounds the sea urchin
embryo.";
                                                           01-MAR-1989 (Rel. 10, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Fibropellin I precursor (Epidermal growth factor-related protein 1)
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SIMILARITY: CONTAINS 21 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 CUB DOMAIN.
SIMILARITY: THE C-TERRINAL DOMAIN OF THIS PROTEIN IS SIMILAR TO AVIDIN/STREPTAVIDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 279-476 AND 781-1064 FROM N.A.
MEDLINE-87319677; PubMed=3448216;
MILSTA D.A., Andrews M.E., Raff R.A.;
"A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 237:1487-1490(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FASEB J. 3:1760-1764(1989).
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                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus.
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                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7668;
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FBP1_STRPU P10079;
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EMBL; L08692; AAA62164.1; -. EMBL; L08692; AAA62163.1; -.

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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                           PROSITE; PS00022; EGF_1; 19.
PROSITE; PS00577; AVIDIN; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF_2: 9.
PROSITE; PS01187; EGF_CA; 19.
Biotin; Alternative splicing; EGF-like domain; Repeat; Signal;
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EMBL; X17530; CAA35571.1; -.
EMBL; M17421; AAA30550.1; -.
EMBL; X17533; CAA35573.1; -.
FIR; A29316; A29316.
HSSP; P07204; 1FGD.
HSSP; P07204; 1FGD.
InterPro; IPR000163; Asx_hydroxyl.
InterPro; IPR000169; Avidin.
InterPro; IPR00059; CUB.
InterPro; IPR00059; CUB.
InterPro; IPR00059; EGF_1ike.
InterPro; IPR001618; EGF_2.
InterPro; IPR001618; EGF_2.
InterPro; IPR00143; EGF_1.
InterPro; IPR00143; EGF_2.
InterPro; IPR00143; EGF_1.
Ffam; FP001382; Avidin; 1.
Ffam; PF000431; CUB; 1.
Ffam; PF000431; CUB; 1.
Ffam; PF000010; EGFBLOOD.
FRINTS; PR00010; EGFBLOOD.
FRINTS; PR00010; EGFBLOOD.
FRINTS; PR00011; EGFELOOD.
FRINTS; PR00011; EGFELOOD.
                                                                                                                                                                                                                            SMART; SM00042; CUB; 1.
SMART; SM0179; EGF_CA; 18.
SMART; SM00001; EGF_like; 3.
PROSITE; PS00010; ASX_HYDROXYL; 19.
                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Calcium-binding.
SIGNAL 1 19 P
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   053533;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Streptavidin V2 precursor (SA V2).
Streptomyces violaceus (Streptomyces venezuelae).
Bacteria; Firmicutes; Actinobacteria; Actinobacterides; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-95359204: pubMed-7632734;
MEDLINE-95359204. r., Adar R., Milchek M.;
"Close similarity among streptavidin-like, blotin-binding proteins from Streptomyces.";
                                                                                                                                                                                                                                            NOT KNOWN
                                                                                                                                                                                                                        Biochim. Biophys. Acta 1263:60-66(1995).
-!- FUNCTION: THE BIOLOGICAL FUNCTION OF STREPTAVIDIN IS NOT KNOWN FORMS A STRONG NON-COVALENT SPECIFIC COMPLEX WITH BIOTIN (ONE MOLECULE OF BIOTIN PER SUBBNIT OF STREPTAVIDIN).
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INVOLVED IN BIOTIN BINDING (BY
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INVOLVED IN BIOTIN BINDING (BY
SIMILARITY).
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-:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
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INVOLVED IN BIOTIN BINDING
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InterPro: IPR000088; Avidin.
Prodom; PF01362; Avidin; 1.
Prodom; PD016055; Avidin; 1.
PROSITE; PS00577; AVIDIN; 1.
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Best Local Similarity 33.64
Matches 43; Conservative
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151 HDTFTKVK 158
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=90036835; PubMed=2808345;
Wingate V.P.M., Broadway R.M., Ryan C.A.;
Isolation and characterization of a novel, developmentally regulated proteinase inhibitor I protein and cDNA from the fruit of a wild
                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 264:17734-17738(1989).
-!- SIMILARITY: BELONGS TO THE POTATO CHYMOTRYPSIN INHIBITOR I FAMILY OF SERINE PROTEASE INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-ANG-1992 (Rel. 23, Last annotation update).
01-ANG-1902 (Rel. 23, Last annotation update).
Wound-induced proteinase inhibitor I precursor.
Lycopersicon peruvianum (Peruvian tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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PIR; A34359; A34359.
HSSP; P19873; HYM.
InterPro; IPR000864; Potato_inhibit.
Ffam; PF00280; potato_inhibit; 1.
PRINTS; PR00292; POTATOINHBTR.
PROSITE; PS002084; POTATO_inhibit; 1.
PROSITE; PS002085; POTATO_inhibit; 1.
PROSITE; PS002085; POTATO_INHIBITOR; 1.
SGTING protease inhibitor; Signal.
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37 111 WOU
87 88 REZ
111 AA; 12610 MW; 3
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Search completed: September 17, 2002, 15:43:39 Job time: 125 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 17, 2002, 15:40:34 Run on:

Search time 16.48 Seconds
(without alignments)
938.737 Million cell updates/sec

Perfect score:

US-09-743-690-7 845 1 MESKFAHIIVFFLLATPFET......DWKATRVGINIFTRLRTQKE 161 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	avidin precursor [avidin-related pro	avidin-related pro	avidin-related pro	avidin-related pro				proteinase inhibit	streptavidin v1 pr	streptavidin precu	\mathbf{H}	streptavidin v2 pr	trypsin inhibitor	fibropellin C prec	serine proteinase	proteinase inhibit	gene atpA intron 1	hypothetical prote	DNA polymerase III	translation elonga	protein C43E11.11	internalin, probab	homeotic protein P	pregnancy-specific	hypothetical prote	hypothetical ser-t	probable membrane	unknown protein, 2
ID	VICH	S42204	S42203	S42201	S42202	806251	S25159	S26717	A24048	S57284	A23513	A40136	S57285	A34359	A48836	S66278	S24979	S25997	T21550	T00615	C26956	A87754	AD1427	S19010	A54879	T00072	T38003	05	G96655
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H71062	A86685	T29545	S52781	H83484	T15606	T43452	S49541	T04722	E86790	T27706	T49500	T21652	B75480	T33881	T33880
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693	1441	974	1268	424	527	684	872	531	725	1250	1421	336	481	575	578
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7.5	75	74.5	74.5	74	74	74	74	73.5	73.5	73.5	73.5	73	72.5	72.5	72.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1
 avidin precursor [validated] - chicken
C.bate: 24-Apr-1984 #sequence_revision 04-Nov-1994 #text_change 15-Sep-2000 C.Bate: 24-Apr-1984 #sequence_revision 04-Nov-1994 #text_change 15-Sep-2000 C.Accesion: A54975: A27518: A92093: A92092: A01160
R;Wallen, M.J.; Laukkanen, M.O.; Kulomaa, M.S. submitted to GenBank, January 1994
A; Description: Sequence of the chicken egg-white avidin gene.
A. Molecular Lives - Mark
 A/Residues: 1/PC. Un A/Residues: 1-21,/5/,23-152 <wal> A/Crocards: 1-21,/5/,000 (PE:100)</wal>
 A;Note: difference at position 22 may be due to PCR error in gene sequence R;Gope, M.L.; Keinaenen, R.A.; Kristo, P.A.; Conneely, O.M.; Beattie, W.G.; Zarucki-S
Nucleic Acids Res. 15, 3595-3606, 1987 A.Title: Molecular cloning of the chicken avidin cont
A; Ille: Molecular clouding of the chicken aviain come. A; Reference number: A27518; MUID:87203384
A. Accession: A27518
A; Molecular Lype: minnA A; Residues: 1-152 <gop></gop>
A; Cross-references: GB: X05343; NID: 963071; PIDN: CAA28954.1; PID: 963072
R:DeLange, R.J.; Huang, T.S.
J. D.D CHEMI. 240, 030-070, 131. Sequence of the 78-residue middle cyanogen bromide per A.Title: Equ white avidin. III. Sequence of the 78-residue middle cyanogen bromide pe
 A; Accession: A92093
A;Molecule type: protein A:Residues: 25-57, T',59-76, E',78-152
 A; Note: approximately 50% of the chains have 58-1le
R.Huang, T.S.; DeLange, R.J. T. Riol Chem. 246, 686-697, 1971
A; Title: Egg white, avidin. II: Isolation, composition, and amino acid sequences of th
 A. Reference number: A95092; Mulb:71107557 A. Acataste: acquisance of trustic martides
 A.Accession: 492092
 A; Molecule type: protein
A: McStudes: 2, 2, 1, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
submitted to the Brookhaven Protein Data Bank, April 1993
 A;Contents: annotation; X-ray crystallography, 3.0 angstroms, With Diotin, residues Z R;Livnah, O.; Bayer, E.A.; Wilchek, M.; Sussman, J.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 5076-5080, 1993
A; Reference number: A47554; MUID:93281699
A; Contents: annotation; X-ray crystallography, 3.0 angstroms
K;rdg.Lese, L; Coda, A;; MalcOvatt, M; BoLognest, M; submitted to the Rrockhaven Protein Data Bank, March 1993

 $\stackrel{\cdot \cdot}{\vdash}$

Gaps

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Indels

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342203
avidin-related protein 3 precursor - chicken
NiAlternate names: avr3 proteil
NiAlternate names: avr3 proteil
C:Species: Gallus gallus (chicken)
C:Species: Gallus gallus (chicken)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-may-1999
C;Accession: 542203; S39800
R:Keinaenen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.; Heleni
Eur. J. Biochem. 220, 615-621, 1994
A;Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-
A;Accession: 542203
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A Molecule type: DNA
A Residues: 1-150 Kers-
A Residues: 1-150 Kers-
A Residues: T-150 Kers-
B R Kunnas, T.A.; Wallen, M.J.; Kulomaa, M.S.
B Biochim. Biophys. Acta 1216, 441-445, 1993
A FILE: Induction of chicken avidin and related mRNAs after bacterial infection.
A R Reference number: S39799; MUID:94092737
A RACCESSION: S39800
                                                                                                                                                                                                                                       30 PEIPARKCSLTGKWTNDLGSNWTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI 89
   Best Local Similarity 75.0%; Fred, No. 1e-41;
Matches 99; Conservative 8; Mismatches 23;
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                     A; Concents: annotation; X-ray crystallography, 2.7 angstroms, with blotin, residues 27-5 R; Pugliese, L.; Coda, A.; Malcovati, M.; Bolognesi, M. submitted to the Brookhaven Protein Data Bank, March 1993
A; Reference number: A31623; PDB:1AVE
A; Contents: annotation; X-ray Crystallography, 2 8 angstroms, without biotin, residues 2
B; Pugliese, L.; Coda, A.; Malcovati, M.; Bolognesi, M.
A; Contents: annotation; X-ray Crystallography, 2 8 angstroms, without biotin, residues 2
B; Pugliese, L.; Coda, A.; Malcovati, M.; Bolognesi, M.
A; Reference number: A34974; MUID:93294833
A; Reference number: A34974; MUID:93294833
A; Contents: annotation; X-ray crystallography, 2.7 angstroms
C; Genetics: A34974; Muid: Muid: Astallography, 2.7 angstroms
C; Reywords: glycoprotein
C;
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Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: 13-3an-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
Cistocession: 842204 $42205
Rikeinaenen, 8.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Tolmela, T.A.; Helenius, Eur. J. Biochem. 220, 615-621, 1994
A.Fitle: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5.
A.Reference number: $42204
A.Recession: 842204
A.Accession: 842204
A.Accession: Lype. DNA
A.A.Olecular type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DCLSARKCSLTCKWTNDLCSNWTIGAVNSRGEFTGTYITAVTATGTSDLHCTQNTI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEIDARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns. 27/3; 96/1; 136/2
G;Genetics: <CH2>
A;Gene: avr5
A;Introns: 27/3; 96/1; 136/2
G;Superfamily: avidin
F;1-24/Domaln: signal sequence #status predicted <SIG>
F;25-150/Product: avidin-related protein 4/5 #status predicted <MAT>
F;28-105/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 684, DB 1; Length 152,
Pred. No. 7.3e-60;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-150 <KEI>
A; Cross-references: EMBL: Z22883; NID: 9311811
A; Experimental source: strain White Leghorn; tissue oviduct
A; Reference number: A51622; PDB:1AVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.98;
97.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
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s42201
avidin related protein 1 precursor - chicken
N.Alternate names: avr1
c; Species: Gallus gallus (chicken)
C; Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 NKRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 PSLSARKCSLTGKWTNNLGSIMTIRAVNSRGEFAGTXLTAVADNPGNIKLSPLIGIOH-- 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 PEIDARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESDLHGTONTI 89
                                                                                                                                                                  A; Introns: 27/3; 96/1; 136/2
C; Superfamily: avidin
F: 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-150/Product: avidin related protein 3 #status predicted <MAT>
F; 28-105/Disulfide bonds: #Status predicted
                                                                                                                                                                                                                                                                                                                                                                                                      Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                      55.5%; Score 469; DB 2;
69.7%; Pred. No. 9.1e-39;
ive 11; Mismatches 27
A; Modecule Lype: mRNA
A; Residues: 71-150 <KUNN
A; Cross-references: EMBL:221536; NID:g65429
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59.1%; Score 499; DB 2; Length 150;

Query Match

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1;

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proteinase inhibitor I precursor - potato (cv. Russet Burbank)
C;Species: Solanum tuberosum (potato)
A;Variety: cv. Russet Burbank
C;Date: 28-Eeb-1990 #sequence_revision 19-Apr-1996 #text_change 16-Jul-1999
C;Accession: S06251; S60563
R;Cleveland, T.E.; Thornburg, R.W.; Ryan, C.A.
Plant Mol. Biol. 8, 199-207, 1987
A;Title: Molecular characterization of a wound-inducible inhibitor I gene from potato A;Reference number: S06251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule Type: DNA
A; Residues: 1-107 CCLES.
A; Sessidues: 1-107 CCLES.
A; Cross-references: EMBL:M17108; NID:g169492; PIDN:AAA33816.1; PID:g169493
A; Experimental source: cultivar Russet Burbank
A; Note: the authors translated the codon CAA for residue 45 as Glu, TCT for residu
B; Sebb, L.J.; Yang, Y.S.
Korean J. Bot. 33, 303-307, 1990
A; Title: Nucleotide sequence of a truncated proteinase inhibitor I gene of potato.
A; Reference number: S60563
A; Reference number: S60563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PotI
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C;Species: Solanum tuberosum (potato)
A;Variety: cultivar llam Hardy
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
C;Accession: S25159; S25470
R;Beuning, LL.; Christeller, J.T.
R;Beuning, LL.; Christeller, J.T.
A;Description: Nucleotide seq of a cDNA encoding the proteinase inhibitor Po
                                                                                                                                                                     Gaps
                                                             PEIPARKCSLIGKWINDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI 89
        Gaps
                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
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f1-123/Domain: signal sequence #status predicted <SIG>
F;24-36/Domain: propeptide #status predicted <PRO>
F;37-107/Product: proteinase inhibitor I #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 107;
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     Indels
     31;
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Pred. No. 4.9e-08;
5; Mismatches 10;
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-14 <SEO>
A;Cross-references: EMBL:Z12819
A;Experimental source: cultivar Russet Burbank
     12;
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Best Local Similarity 63.5%;
Matches 33; Conservative
     Conservative
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A; Accession: S25159
                                                                                                                                                                                                                                                                                    150 INIFTRLRTQKE 161
                                                                                                                                                                                                                                                                                                                                           139 NNDFTRQHTVEE 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
87;
                                                             30
     Matches
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S25159
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C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Accession: S42202; S39799
K; Kainaenen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.; Helenius, Bur. J. Blochem. 220, 615-621, 1994
A; Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5. A; Reference number: S42201; MUID:94170814
A; Reference number: S42202
A; Status: preliminary
                             R;Keinaenen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.; Helenius, Eur. J. Blochem. 220, 615-621, 1994
ArTitle: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5. A;Reference number: $42201; MUID:94170814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Rolecule type: DNA
A.Residues: 1-150 <KEL>
A.Cross-references: EMBL: 221554; NID:965430
R.Kunnas, T.A.; Wallen, M.J.; Kulomaa, M.S.
Biochim. Biophys. Acta 1216, 441-445, 1993
A.Title: Induction of Chicken avidin and related mRNAs after bacterial infection.
A.Reference number: S39799; MUID:94092737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEIPARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 PGLSARKCSLTGKWDNDLGSIMTIGAVNDNGEFNGTYITAVADNPGNITRSPLLGIQH--- 78
                                                                                                                                                                                                                                                                                                     A Introns: 27/3; 96/1; 136/2
C; Superfamily: avidin
C; Superds: glycoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-150/Product: avidin-related protein 1 #status predicted <MAT>
F:28-105/Disulfide bonds: #status predicted
F:54,67,93/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-150/Product: avidin-related protein 2 #status predicted <MAT>
F;28-105/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 458; DB 2;
; Pred. No. 1.1e-37;
11; Mismatches 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 444; DB 2;
Pred. No. 2.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      avidin-related protein 2 precursor - chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.2%;
Best Local Similarity 67.4%;
Matches 89; Conservative 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.5%;
65.9%;
                                                                                                                                                                                                                                              A; Cross-references: EMBL: Z21611
C; Genetics:
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139 NNDFTRORTVEE 150
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Best Local Similarity
                                                                                                                                                                                                                       A; Residues: 1-150 <KEI>
                                                                                                                                     A; Accession: S42201
A; Status: preliminary
A; Molecule type: DNA
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residue

1;

C;Genetics: A;Gene: avr2

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streptavidin v1 precursor - Streptomyces venezuelae
GiSpecies: Streptomyces venezuelae
Ribaryer, E.A.; Kulik, T.; Adar, R.; Wilchek, M.
Ribayer, E.A.; Kulik, T.; Wilchek, M.
Ribayer, E.A.; Kulik, M.
Ribayer, M.
Ribaye
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R;Gitlin, G.; Bayer, E.A.; Wilchek, M.
Biochem, J. 269, 527-530, 1990
A;Title: Studies on the biotin binding sites of avidin and streptavidin, Tyrosine res A;Reference number: S11540; MUID:90351377
on modification of proteins that are sequestered within cellular storage vacuoles. C.Superfamily: eglin C
C.Keywords: serine proteinase inhibitor
F;1-23/Domain: signal sequence #status predicted <SIG>F;24.4.0.Domain: propeptide #status predicted <PRO>F;24.4.0.Domain: propeptide #status predicted <PRO>F;43-111/Product: proteinase inhibitor I #status predicted <MAT>F;87/Inhibitory site: Lew (Chymotrypsin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptavidin precursor - Streptomyces avidinii
C.Species: Streptomyces avidinii
C.Species: Streptomyces avidinii
C.Species: Streptomyces avidinii
C.Species: 03-Nov-1987 #sequence_revision 03-Nov-1987 #text_change 11-Jan-2002
C.Accession: A23513; S11540
R.Accession: A23513; S11540
Nucleic Acids Res. 14, 1811-1882, 1986
A;Title: Molecular cloning and nucleotide sequence of the streptavidin gene. A;Reference number: A23513; MUID:86148514
A;Accession: A23513; MUID:86148514
A;Gtatus: preliminary
A;Molecule Lype: DNA
A;Residues: 1-183 AARC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 GSGT--ALGWIYAWKNNYRNAHSAIIWSGQYY---GGIEARINIQWLLISGIIE-ANAWK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caps
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                                                                                                                                                                                                                                                                                                                                                                                 Length 111;
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(Superfamily: Streptavidin
E:1.24/Domain: signal sequence #status predicted <SIG>
F:25-183/Froduct: streptavidin v1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                      Query Match 16.9%; Score 142.5; DB 2; Best Local Similarity 32.3%; Pred. No. 1.3e-06; Matches 43; Conservative 20; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MESKFAHIIVFFLLATPFETLLARKESDGPEI 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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STLVGHDTFTKVK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 ATRVGINIFTRLR 157
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
28, Conserv
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
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N.Alternate names: wound-induced proteinase inhibitor I
C.Specias: Lycopersion esculation
C.Specias: Lycopersion esculation
C.Spate: 05-Jun-1907 #sequence_revision 05-Jun-1967 #text_change 21-Jul-2000
C.Accession: A25046; A24048
R.Lee, J.S.; Barown, W.B.; Graham, J.S.; Pearle, G.; Pox, E.A.; Dreher, T.W.; Ahern, K.G.
Proc. Natl. Acad. Sci. U.S.A. 83, 7277-7281, 1966
A.TILLE: MOLECULAR Characterization and phylogenetic studies of a wound-inducible protein
A.Reference number: A25046
A.Molecule type: DNA
A.Residues: 1-111 < LEB
A.Cross-references: GB.M1938; NID:g170519; PIDN:AAA34200.1; PID:g170520
A.Experimental source: tomato leaves, cv. Bonny Best
A.Cross-references: GB.M1938; NID:g170517; PIDN:AAA34200.1; PID:g170518
A.Reference number: A92531; MUD:85207657
A.Reference number: A32331; MUD:85207657
A.Residues: 1-11 < GRA>
A.Recssion: A34048
A.Recssion: A34048
A.Recssion: A34048
A.Recsion: A34048
A.Recsion: A34048
A.Recsion: A14048
A.Recsion: A140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:CAA78259.1; PID:921559 for residue 42 as Asn and CTA for residue
                                                                                                                                                                                                                                                              6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteinase inhibitor I precursor - potato
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                         Length 107
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                     Score 151; DB 2;
Pred. No. 9.7e-08;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MESKFAHIIVFFLLAFSFETLARKESDGDEV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MESKFAHIIVFFLLATPFETLLARKESDGPEI 32
            C;Superfamily: eglin C
C;Keywords: serine proteinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.9%;
87.5%;
                                                                                                                                                                         17.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: $26717
R; Lee, J.S.; Park, J.S.
Rorean J. Bot. 32, 67-78, 1989
                                                                                                                                                                                                                    Best Local Similarity 93.8
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28; Conservative
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Best Local Similarity
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F;23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261
57 451-466,468-477,48-4795/Disulfide bonds: #status predicted
F;489-504,506-515,522-53,527-55,544-555,560-571,565-580,582-591,598-609,603-618,620
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Streptomyces venezuelee
C;Date: 19-Mar.1997 #sequence_revision 19-Mar.1997 #text_change 10-Dec-1999
C;Accession: S57281
R;Bayer, E.A.; Kullk, T.; Adar, R.; Wilchek, M.
Biochim. Biophys. Acta 1263, 60-66, 1995
A;Title: Close similarity among streptavidin-like, biotin-binding proteins from Strep A;Reference number: S57284; MUID:95359204
A;Accession: S57285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        990 NYDFPSFGFTVVRDNGQSTTSWTGQCHL-CDGEEVLYTTWINTNWVSTCQDIKKSNWVGQ 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 KRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVGI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 PTFGFTVNWK----FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 CSLTGKWINDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI-----N 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 KCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHGTQNTINKRTQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 EAGITGTWYNQLGSTFIVTA-NADGSLTGTYESAVGNAESRYVLTGRYDSAPATDGSGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.6%; Score 140; DB 2; Length 1064; 33.6%; Pred. No. 2.1e-05; ive 16; Mismatches 51; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Experimental source: strain Tue2605
Subperfamily: streptavidin
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-183/Product: streptavidin v2 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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Best Local Similarity 33.6%; Pred. No. 2.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               streptavidin v2 precursor - Streptomyces venezuelae
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                                                                                                                                                                                                                       <EG11><EG12><EG13><EG14>
                                                                                                                                                                        <EG10>
                                                                                                                                                                                                                                                                                                                              <EG15><EG16>
                                                                                                                                                                                                                                                                                                                                                                               <EG17>
                                                                                                                      <EG07>
                                                                                                                                                                                                                                                                                                                                                                                                                                 <EG19>
                                                                         <EG05>
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Best Local Similarity 33.69
Matches 42; Conservative
homology
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A; Residues: 1-183 <BAY>
                                                                                              EGF
EGF
EGF
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F;864-895/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;902-933/Domain:
                                                                                                                                                                                                                                                       F;560-591/Domain:
F;598-629/Domain:
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F;788-819/Domain:
F:180-211/Domain:
                                                                                                 F;332-363/Domain:
                                                                                                                      F;370-401/Domain:
                                                                                                                                                   F;408-439/Domain:
                                                                                                                                                                          /Domain:
                                                                                                                                                                                                     F;484-515/Domain:
                                                                                                                                                                                                                               522-553/Domain:
                                                                                                                                                                                                                                                                                                        F;636-667/Domain:
                                                                                                                                                                                                                                                                                                                                F;674-705/Domain:
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                                                                         F; 294-325/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N; Alternate names: epidermal growth factor homolog precursor
N; Contains: alternatively spliced fibropellin ID (EGFI)
C; Species: Strongylocentrotus purpuratus (purple urchin)
G; Species: Strongylocentrotus (A0136; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J; Mol. Evol. 29, 314-327, 1989
A; Title: Structural analysis of the uGF gene in the sea urchin Strongylocentrotus purpu
A; Reference number: A40136; MUID:90112459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Status: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 'K', 747-821,898-978 < DE3>
R; Hursh, D.A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987
A; Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A; Reference number: A29316; MUID:87319677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Molecule type: mRNA
A; Residues: 'S', 280-481,786-1064 <HUR>
A; Cross-references: GB:M17421; NID:9161474; PIDN:AAA30050.1; PID:9552260
R; Hunt, L.T.; Barker, W.C.
FASEB J. 3, 1760-1764, 1989
A;Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.
                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSGT--ALGWIVAWKNNYRNAHSATIWSGQYV---GGAEARINTQWLLITSGTTE-ANAWK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 NKRTQPTFGFTVNWK----FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWK 144
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                               31 EIPARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                              Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:X17530; NID:g10225; PID:g667061
A;Accession: B40136
A;Status: prellminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>
                                                                                                                                                                                                                                                                                                                                57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: CIr/CIS repeat homology; EGF homology
F;1-19-7Domain: signal sequence #status predicted <51G>
F;20-1064/Product: [ibropellin I #status predicted <FIB>
F;23-54/Domain: EGF homology; <EG01>
                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                        .3e-06;
                                                                                                                                                                     F;67/Binding site: biotin (Tyr) #status predicted F;78/Binding site: biotin (Tyr) #status predicted
                                                                                                                      F;1-24/Domain: signal sequence #status predicted F;25-183/Product: streptavidin #status predicted
                                                                                                                                                                                                                                                                         16.9%; Score 142.5;
32.3%; Pred. No. 1.3e
Live 20; Mismatches
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A; Contents: annotation
                                                                                           :Keywords: biotin binding; homotetramer
             A, Molecule type: protein
A, Residues: 54-66, X', 68 <GIT>
C, Superfamily: streptavidin
                                                                                                                                                                                                                                                                                                                              43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STLVGHDTFTKVK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 ATRVGINIFTRLR 157
                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 43; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-114 <DEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: C40136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A29316
                                                                                                                                                                                                                                                                            Query Match
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7;

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Job time: 133 sec
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fibropellin C precursor - sea urchin (Strongylocentrotus purpuratus)
NiAlternate names: ECF repeat-containing profedin; epidermal growth
NiAlternate names: ECF repeat-containing profedin; epidermal growth
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Accession: A48836
R:Bisgrowe, B. W.; Raff, R.A.
Dev. Biol. 157, 526-538, 1993
A-Title: The SpECF III gene encodes a member of the fibropellins: EGF repeat-containing
A:Reference number: A48836
A:Accession: A48836
A:Access
                                                                                                                                                                                                                                                                                                                                             Anylogic inhibitor I precursor - Peruvian tomato
C; Species: Lycopersicon peruvianum (Peruvian tomato)
C; Species: Lycopersicon peruvianum (Sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
C; Accession: A39547; M3059
A; Wingate, V.P.M.; Ryan, C.A.
A; Reference number: A39547; MUID: 91170261
A; Rittle: A novel fruit-expressed trypsin inhibitor I gene from a wild species of tomato.
A; Reference number: A39547; MUID: 91170261
A; Reference number: A39547; MUID: 91170261
A; Reference number: BMS947
A; Reference number: BMS9427
A; Note: the authors translated the codon AAA for residue 37 as Ile, GAC for residue 42 a A; Note: the authors translated the codon AAA for residue 37 as Ile, GAC for residue 42 a A; Note: the authors and characterization of a novel, developmentally regulated proteinase A; Reference number: A34359; MUID: 90036835
A; Status: Preliminary
A; Rocession: A34359; MUID: 90036835
A; Residues: Preliminary
A; Residues: 1-11 (WIZ)
A; Residues: 1-11 (WIZ)
A; Residues: 1-11 (WIZ)
A; Residues: GB: M10 (C)
C; Superfamily: eglin C
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-ALCWTVAWKNNYRNAHSATTWSGOYVA---GSEARINTOWLLTSGTT-AANAWKSTLYG 150
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4; Mismatches
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Les 26, Conservative
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151 HDTFTKVK 158
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Search completed: September 17, 2002, 15:42:47

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(without alignments)
303.670 Million cell updates/sec
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7, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, 18 Sequence 7, 18 Sequence 7, 18 Sequence 9, 18 Sequence 2, 18 Sequence 16, 18 Sequence 17, 18 Se
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Sequence 17, A
Sequence 1, Ap
Sequence 5, Ap
                                                                                                                          ; Search time 12.95 Seconds
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1 MESKFAHIIVFFLLATPFET......DWKATRVGINIFTRLRTQKE 161
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/cgn2_6/ptodata/2/iaa/5B_COWB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COWB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COWB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
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US-08-628-540-1
US-08-941-100-1
US-08-941-100-5
US-08-931-399-2
PCT-US93-05240-14
5168049-5
US-08-491-988-7
US-08-491-988-9
US-08-831-399-16
US-08-831-399-16
US-08-831-399-16
US-08-752-3078-7
US-08-752-3078-7
US-08-752-3078-7
US-08-752-3078-7
US-08-753-94-1
US-08-428-94-84-1
US-08-428-94-94-1
US-08-233-008A-2
US-08-233-008A-2
US-08-233-008A-2
US-08-233-008A-2
US-08-923-008A-2
US-08-923-008A-2
US-08-923-008A-2
US-08-923-008A-2
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US-08-923-008A-2
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                                                                                                                     September 17, 2002, 15:39:39
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Maximum Match 100%
Listing first 45 summaries
                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                       US-09-743-690-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length
                   Copyright
                                                                                                                                                                                                                                                                                                                                                                                               Fotal number of
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66.5
66.5
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66
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Perfect score:
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142.5
142.5
142.5
142.5
142.5
142.5
141.1
135.5
135.5
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                                                                               OM protein
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                                                                                                                        Run on:
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APPLICANT: Kopetzki, Erhard; Muller, Rainer;
APPLICANT: Engh, Richard; Schmitt, Urban; Deger, Arno; Brandstetter, Hans TITLE OF INVENTION: Recombinant Inactive Core TITLE OF INVENTION: Streptavidin Mutants
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
                           Appli
                           Sequence
                                                  Sequence
Sequence
Sequence
Sequence
                                                                                                  Sequence
                                                                                                                         Sequence
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Sequence
Sequence
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Pred. No. 2.2e-73;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
US-08-340-428B-49
US-08-292-549-2
US-09-042-785A-9
PCT-US91-02207-2
US-08-317-522A-3
US-08-751-965-3
US-08-738-975-3
US-08-738-975-3
US-08-738-975-3
US-08-17-522A-2
US-08-17-522A-2
US-08-17-522A-2
US-08-728-626-2
US-08-738-975-2
US-08-738-975-2
US-08-738-975-2
US-08-728-626-2
US-08-728-626-2
US-08-728-626-2
US-08-728-626-2
US-08-728-626-2
US-08-728-626-2
US-08-728-626-2
US-08-76-967-2
US-08-487-890A-113
                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: 150 PS/2

OCHENTIA SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/831,399
FILING DATE: 1-April-1997
CLASSIFICATION:
PRIOR APPLICATION NUMBER: DE 196 13 053.0
FILING DATE: 1-April-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 37 718.8
FILING DATE: 1-April-1996
PRIOR APPLICATION NUMBER: DE 196 37 718.8
FILING DATE: 16-September-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hanson, No. 6312916man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: HUBR 1105
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08831399
Patent No. 6312916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-384
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 80.9%;
Best Local Similarity 97.7%;
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 152 amino acids
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   amino
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Gaps

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90 NKRTQPTFGFTVNWK----FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWK 144
                                                                                                          68 GSGT--ALGWTVAWKNNYRNAHSATTWSGQYV---GGAEARINTQWLLTSGTTE-ANAWK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 NKRTQPTFGFTVNWK----FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 GSGT--ALGWTVAWKNYRNAHSATTWSGQYV---GGAEARINTQWLLTSGTTE-ANAWK 121
31 EIDARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHGTQNTI 89
                                          29
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                        DB 3; Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08941100B
| Patent No. 6207390 | GENERAL INFORMATION: GARLEANT: Cantor, Charles R. APPLICANT: Cantor, Charles R. APPLICANT: Sano, Takeshi | TITLE OF INVENTION: Reduced Affinity Streptavidin | FILE REFERENCE: BU-03165 | CURRENT APPLICATION NUMBER: US/08/941,100B | CURRENT FILING DATE: 1997-10-03 | PRIOR FILING DATE: 1995-06-06 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.9%; Score 142.5; DB 3 32.3%; Pred. No. 3.3e-09; tive 20; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: SKETTA, AINE
APPLICANT: SKETTA, AINE
TITLE OF INVENTION: Streptavidin Muteins;
FILE REFERENCE: HUBR 1119
CURRENT APPLICATION NUMBER: US/08/948,097C
CORRENT FILING DATE: 1997-10-09
EARLIER FILING DATE: 1996-10-10
HUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/420,010
PRIOR PILING DATE: 1995-04-11
                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08948097C Patent No. 6103493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; OKGANISM: Streptomyces avidinii
US-08-948-097-17
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TYPE: PRT
ORGANISM: Streptomyces avidinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS; 5
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Conservative
                                                                                                                                                                     145 ATRVGINIFTRLR 157
                                                                                                                                                                                              :| || : ||:::
122 STLVGHDTFTKVK 134
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122 STLVGHDTFTKVK 134
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US-08-948-097-17
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LENGTH: 159
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US-08-941-100-1
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                                                                                                       90 NKRIQPIFGFIYNMKFSESTIYFIGQCFIDRNGKEYLKIMMLLRSSYNDIGDDWKATRYG 149
30 PEIDARKCSLTGKWTNDLGSNMTICAVNSRGEFTGTYITAVTATSNEIKESDLHGTONTI 89
                      1 PGLSARKCSLTGKWTNDLGSNWTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PANDORI, MARK W.
TITLE OF INVENTION: STREPTAVIDIN MUTANTS
NUMBER OS SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               016865-0244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,540
FILING DATE: 10-APR-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/420,010
FILING DATE: 11-APR-1995
APPLICATION NUMBER: 60/003,687
FILING DATE: 18-SEP-1995
ATTORNET/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          US-08 628-540-1
Sequence 1, Application US/08628540
Fatent No. 6022951
GENERAL INFORMATION:
APPLICANT: SANO, Takeshi
APPLICANT: CANTOR, Charles R.
APPLICANT: VADDA, Sandor
APPLICANT: REZNIK, Gabriel O.
APPLICANT: SMITH, Cassandra L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Remenick, James
REGISTRAGION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 016
TELECOMMUNICATION INFORMATION:
TELEDHONE: 202-639-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 159 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 32.3?
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-639-7890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              150 INIFTRLRTOKE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004-2400
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Patent No. 6312916
GENERAL INFORMATION: APPLICANT: Engh, Richard; Muller, Rainer; Arno; Brandstetter, Hans APPLICANT: Engh, Richard; Schmitt, Urban; Deger, Arno; Brandstetter, Hans
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                                                                                                                                                                                                                                                                                    90 NKRTQPTFGFTVNWK----FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWK 144
                                                                                                                                                                                                                                                                                                           68 GSGT--ALGWTVAWKNNYRNAHSATTWSGQYV---GGAEARINTQWLLTSGTTE-ANAWK 121
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                                                                                                                                                                                                       31 EIPARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                              : LOCATION: (1)

; OTHER INFORMATION: The residue in this position can be any amino is OTHER INFORMATION: acid.
US-08-941-100-1
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                                                                                                                         Length 159;
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A REPLICANT: Cantor, Charles R.
APPLICANT: Sano, Takeshi
TITLE OF INVENTION: Reduced Affinity Streptavidin
FILE REFERENCE: BU-03165
CURRENT APPLICATION NUMBER: US/08/941,100B
CURRENT FILING DATE: 1997-10-03
PRIOR APPLICATION NUMBER: 08/469,353
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/469,353
PRIOR FILING DATE: 1995-04-11
NUMBER OF SEQ ID NOSE: 5
                                                                                                                         DB 4;
                                                                                                                       16.9%; Score 142.5; DB 4
32.3%; Pred. No. 3.3e-09;
Live 20; Mismatches 57
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32.3%; Pred. No. 3.3e-09;
Live 20; Mismatches 57
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Patent No. 6207390
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US-08-941-100-5
                                                                                                                     Query Match
Best Local Similarity 32.3%
Matches 43; Conservative
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Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      145 ATRVGINIFTRLR 157
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STLVGHDTFTKVK 134
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US-08-941-100-5
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LENGTH: 159
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90 NKRTQPTFGFTVNWK----FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWK 144
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PCT-US93-05240-14
Sequence 14 Application PC/TUS9305240
GENERAL INFORMATION:
APPLICANT: NAGARAJAN, VASANTHA
TITLE OF INVENTION: PRODUCTION OF STREPTAVIDIN FROM BACILLUS
TITLE OF INVENTION: SUBSTILLIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DU PONT COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Indels
                                                                                                                                                                                           ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
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Recombinant Inactive Core
Streptavidin Mutants
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32.3%; Pred. No. 4e-09;
tive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 13 053.0
FILING DATE: 1-April-1996
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: DE 196 37 718.8
FILING DATE: 16-September-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: HUBR 1105
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         UMBER: US/08/831,399
1-April-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hanson, No. 6312916man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: BARLEY MILL PLAZA 36 CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEC ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                 ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 183 amino acids
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Best Local Similarity 32.39
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 1-April-1
CLASSIFICATION:
                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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146 STLVGHDTFTKVK 158
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TITLE OF INVENTION:
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Gaps

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146 STLVGHDTFTKVK 158
                                                             RESULT 9
US-08-491-988-7
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TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 GSGT--ALGWIYAMKNNYKNAHSATIWSGQIY---GGAEARINIQWLLISGTIE-ANAWK 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 16.9%; Score 142.5; DB 5; Length 183; Best Local Similarity 32.3%; Pred. NO. 4e-09; Matches 43; Conservative 20; Mismatches 57; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MEADE, HARRY M.; GARWIN, JEFFREY L.
TITLE OF INVENTION: PRODUCTION OF STREPTAVIDIN-LIKE
                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.9%; Score 142.5; DB 6; 32.3%; Pred. No. 4e-09; tive 20; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/185,329
FILING DATE: 21-AFR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 656,873
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    NAME: GELGER, KATHLEEN W
REFERENCE/DOCKET NUMBER: CR 9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-2118
TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 14:
                                                                                                               FILING DATE: 19930527
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             LENGTH: 183 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-OCT-1984; SEQ ID NO:5:
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                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   unknown
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; MOLECULE TYPE: protein
PCT-US93-05240-14
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146 STLVGHDTFTKVK 158
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Best Local Similarity
Matches 43; Conserva
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;Patent No. 5168049
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285 QVSAAEAGITGTWYNQLGSTFIVTA-GADGALTGTYESAVGNAESRYVLTGRYDSAPATD 343
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                                                                                                                                                                                                                                 ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET; 261 MADISON AYENUE
CITY: NEW YORK
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ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.9%; Score 142.5; DB 2; 32.3%; Pred. No. 1.3e-08;
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APPLICANT: EPENETOS, ACAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
                                                                                                                                                             targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Mismatches
                                                                                                                                                          Compounds for
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                     Patent No. 59†3116
GENERAL INFORMATION:
APPLICANT: BEDENTOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-DEC 1995
CLASSIFICATION: 424
APTORNEY-AGENT INDORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELEPHONE: 212-986-4090
TELEFRAX: 212-818-9479
INPORMATION FOR SEQ ID NO: 7:
; Sequence 7, Application US/08491988
; Patent No. 5973116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-491-988-5; Sequence 5, Application US/08491988; Patent No. 5973116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 415 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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, MOLECULE TYPE: protein
US-08-491-988-7
                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STLVGHDTFTKVK 410
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10016-2391
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REGISTRATION NUMBER: 24,408
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LEMOTH: 402 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 ANAWKSTLVGHDTFTKVK 397
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amino acid
                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-491-988-9
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ZIP: 2005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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STATE: D.C.
COUNTRY: USA
                                                                                                                                                                           linear
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                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 NKRTQPTFGFTVNWK----FSESTTVFTGQCFIDRNGKEV-LKTWWLLRSSVNDIGDDWK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 EIPARKCSLIGKWINDLGSNMTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 435;
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                                                                       COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 4.24
ATTORNEY/ACTION: 4.24
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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32.3%; Pred. No. 1.4e-08;
iive 20; Mismatches 57
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APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
ITILE OF INVENTION: Compounds for targeting
CORRESPONDENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/491,988 FILING DATE: 18-DEC-1995 CLASSIFICATION: 424
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; Sequence 9, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 MADISON AVENUE
261 MADISON AVENUE
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SEQUENCE CHARACTERISTICS:
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ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 435 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Query Match 16.9% Best Local Similarity 32.3% Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-491-988-5
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398 STLVGHDTFTKVK 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                 NEW YORK
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                                                         USA
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                                                         COUNTRY:
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                                 STATE:
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                                                      Gaps
                                                                                                               29 GPEIPA---RKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHG
                                                         16;
Query Match 16.7%; Score 141; DB 2; Length 402; Best Local Similarity 33.3%; Pred. No. 1.9e-08; Matches 46; Conservative 18; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KOPETZKI, Erhard
APPLICANT: RUDOLPH, Rainer
APPLICANT: RUDOLPH, Rainer
APPLICANT: GROSSMANN, Adelbert
ATTLE OF INVENTION: RECOMBINANT CORE STREPTAVIDIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Nikaido, Marmelstein, Murray & Oram STREET: 655 Fifteenth Street N.W., Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 41:35 543.1
FILLING DATE: 28-OCT-1992
ATTORNEY/AGENT INFORMATION:
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Patent No. 5489528
GENERAL INFORMATION:
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Matches

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Sequence 16, Application US/08831399
Patent No. 6312916
GENERAL INFORMATION:
APPLICANT: Kopetzki, Erhard; Muller, Rainer;
APPLICANT: Engh, Richard; Schmitt, Urban; Deger, Arno; Brandstetter, Hans
TITLE OF INVENTION: Recombinant Inactive Core
TITLE OF INVENTION: Streptavidin Mutants
                                                                                                                                    95 PTFGFTVNWK----FSESTTVFTGQCFIDRNGKEY-LKTMWLLRSSVNDIGDDWKATRYG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 PIFGFIVNWK----FSESTIVFIGGCFIDRNCKEV-LKTMWLLRSSVNDIGDDWKATRVC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 -ALGWTVAWKNNYRNAHSATYTWSGOYV---GCAEARINTQWLLTSGTTE-ANAWKSTLVG 115
3 BAGITGTWYNOLGSTPIVTA-GADGALTGTYBSAVGNAESRYVLTGRYDSAPATDGSGT- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 13; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 EAGITGTWYNQLGSTFIVTA-GADGALTGTYESAVGNAESRYVLTGRYDSAPATDGSGT- 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 13 053.0
FILING DATE: 1-APF11-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 37 718.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUBR 1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-September-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6312916man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: HOTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pc-Dos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 128 amino acids
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Best Local Similarity 32.89
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York City
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PS/2 OPERATING SYSTEM: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                   116 HDTFTKVK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                             08-831-399-16
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                95 PTFGFTVNWK----FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                                                                                                                                                                                         3 EAGITGTWINQLGSTFIVIA-GADGALTGTYESAVGNAESRYVLTGRYDSAPATDGSGT- 60
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                     36 KCSLTGKWTNDLCSNMTICAVNSRGEFTGTYITAV-TATSNEIKESPLHGTQNTINKRTQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 KCSLTCKWTNDLCSNWTIGAVNSRGEFTGTVITAV-TATSNEIKESPLHGTQNTINKPTQ 94
                                                                                                                                                           13;
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                                                                                                 DB 1; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.0%; Score 135.5; DB 1; Length 128; 32.8%; Pred. No. 1.6e-08; tive 18; Mismatches 55; Indels 13
                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: DESCRIPTION OF THE WARDEN OF THE W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KOPETZKI, Erhard
APPLICANT: RUDOLDH, Rainer
APPLICANT: RUDOLDH, Rainer
TITLE OF INVENTION: RECOMBINANT CORE STREPTAVIDIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIGO, MARMEISTEIN, MULTAY & OTAM
STREET: 655 Fifteenth Street N.W., Suite 330
CITY: Mashington
                                                                                                                                                           55;
                                                                                          Score 135.5; DB 1 pred. No. 1.6e-08;
                                                                                                                                                           18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-5007
TELECOMMUNICATION:
TELEDHONE: (202) 638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08434718
Patent No. 5672691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEC ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 32.8%
Matches 42; Conservative
                                                                                                                                                        42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE; protein US-08-434-718-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2005-5701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 HDTFTKVK 123
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US-08-211-833-2
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116 HDTFTKVK 123

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RESULT 15
US-08-554-586-2

Sequence 2, Application US/08554586

Sequence 2, Application US/08554586

Bactent No. 5767379

GENERAL INFORMATION:

APPLICANT: HOOD. Elizabeth

APPLICANT: MADDOCK, Sheila

APPLICANT: MESTSTER III, James C.

APPLICANT: MESTSTER III, James C.

APPLICANT: HOWARD, John A.

TITLE OF INVENTION: COMMERCIAL PRODUCTION OF AVIDIN IN

TITLE OF INVENTION: PLANTS

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 13.6%; Score 115; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 3.2e-07; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STREET: 0.C
CITY: Washington
STREET: DOOT-5108
COMPUTER: USA

ZIP: 2007-5108
COMPUTER: ENABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,586
FILING DATE: 06-NOV-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 29,768
RECISTRATION NUMBER: 29,768
RECISTRATION NUMBER: 29,768
RECISTRATION NUMBER: 33229/352/PIHI
TELEPHONE: (202)672-5399
TELEX: (202)672-5399
TELEX: (201)672-5399
TELEX: 21 anino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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34 ARKCSLTGKWTNDLGSNMTIG 54 1 ARKCSLTGKWTNDLGSNMTIG 21 Ω

Search completed: September 17, 2002, 15:42:24 Job time: 165 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 17, 2002, 15:37:39 Run on:

; Search time 30.07 Seconds (without alignments) 594.708 Million cell updates/sec

US-09-743-690-7 Perfect score:

845 1 MESKFAHIIVFFLLATPFET......DWKATRVGINIFTRLRTQKE 161 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

747574 Total number of hits satisfying chosen parameters: 747574 seqs, 111073796 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
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/SIDSI/gcgdata/hold-geneseqygeneseqp-embl/AA1987.DAT:*
/SIDSI/gcgdata/hold-geneseqygeneseqp-embl/AA1987.DAT:* A_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Potato proteinase	Wild-type avidin p	Chicken avidin. G	Amino acid sequenc	Bovine scavenger r	Chicken eqq white	Chicken egg white	Scrv prasiio and p	. S. avidinii strept	Streptomyces avidi	Mature streptavidi
QI	AAY44699	AAW29307	AAY17867	AAY30130	AAY03098	AAB35269	AAB35271	AAR56485	AAW59217	AAB35270	AAP93531
DB	21	18	20	20	20	22	22	15	19	22	10
% Query Match Length DB	161	152	152	152	400	128	128	402	183	159	160
% Query Match	100.0	6.08	6.08	90.6	80.2	79.3	77.6	17.5	17.2	16.9	16.9
Score	845	684	684	681	678	670	959	148	145.5	142.5	142.5
Result No.	н	7	Э	4	5	9	7	80	თ	10	11

99WO-NZ00110. 98NZ-0331002.

15-JUL-1999; 15-JUL-1998;

Streptomyces avidi Streptomyces avidi Biosynthetic prote Streptavidin seque Sequence of a stre Streptavidin prote	Streptavidin gene. Wild type streptav S. avidinii strept Streptococcus stre Streptococcus stre Streptovidin prote	Streptomyces avidi Streptomyces avidi A fusion of anti-C ScFV pRAS109 and p A fusion of anti-C A fusion of single	Scrv pRAS108 and p Streptavidin prote Potato proteinase S. avidinii strept Streptavidin prote Amino acid sequenc Streptavidin prote	Core streptavidin. Streptomyces avidi Recombinant Core·s Streptavidin protein S. avidini protein Streptavidin/lucif Amino acid sequenc Streptomyces avidi Streptomyces avidi
161 21 AAY80515 162 21 AAY80514 163 9 AAP80160 182 8 AAP70492 183 7 AAP60625 183 10 AAP93530	183 14 AAR44491 183 18 AAW59306 183 20 AAY17868 183 21 AAY4701 183 21 AAY4701	22 22 22 22 22	15 18 18 18 18	128 14 AAR34722 128 17 AAW02011 128 18 AAW29308 159 18 AAW29314 270 20 AAY28928 673 17 AAW04208 186 21 AAY84022 122 21 AAY84022 122 21 AAY84022
16.9 16.9 16.9 16.9 16.9	25 25 25 25 25 25 25 25 25 25 25 25 25 2	16.99		16.0 16.0 15.9 15.9
12 13 14 15 17	118 222 224 224	22222 2422 2422 2422 2422 2422 2422 24	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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7...23
/note= "Potato proteinase inhibitor-I signal peptide"
34..161
/note= "Avidin sequence"
                                                                                                           Potato proteinase inhibitor-I; PPI-I; streptavidin; worm; avidin; insect; plant-noxious protein; pest resistance; moth; insect; weevil; grub; beetle; fly; thrip; loust; cricket; borer; mite; looper; insecticidal; fusion protein.
                                                                                                                                                                                                          1.31
/note= "Potato proteinase inhibitor-I sequence"
                                                                                        Potato proteinase inhibitor-I/Avidin fusion protein.
                                                                                                                                                                                                Location/Qualifiers
                       AAY44699 standard; Protein; 161 AA
                                                                  25-APR-2000 (first entry)
                                                                                                                                                                  Solanum tuberosum.
                                                                                                                                                                                                                                                                                    WO200004049-A1.
                                                                                                                                                                                                                                                                                                         27-JAN-2000
                                                                                                                                                                             Synthetic
                                            AAY44699;
                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                      Protein
т
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             AAY44699
   RESULT
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constructed from a core streptavidin or avidin sequence are selected that differ from the native polypeptide by at least one amino acid and have a binding affinity for biotin of less than 1010 l/mole. The biotin-bindable polypeptide may be present as a polymeric conjugate, e.g. with another polypeptide or protein, especially bownes serum albumin. These muteins are used as anti-interference reagents for reducing and/or avoiding nonspecific interactions in a process for detecting an analyte. In specific binding pair is involved for qualitative and/or quantitative determination of an analyte in a test sample, e.g. a heterogeneous affinity for biotin, the muteins assay, Despite having a lower binding a sfinity for biotin, the muteins assay. Despite having a lower binding with native streptavidin and avidin.
                                                                                                                                                                                                                                                                                                            This sequence represents an avidin which is used in a novel method of reducing interference from non-specific binding in assays. Muteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 NKRTQPTFGFTVNWKFSESTTYFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptavidin and avidin muteins with reduced binding affinity for blotin - useful for reducing interference from nonspecific binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 PEIPARKCSLTGKWTNDLGSNWTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTONTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptavidin; batroxobin; fibrinogen converting enzyme; fusion protein; sealant; surgery; reduce bleeding; fibrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.9%; Score 684; DB 18; Length 152; 97.7%; Pred. No. 7.6e-66;
                                                                Kopetzki E, Mueller R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                   Disclosure; Page 19-20; 26pp; German.
                                                                Brandstetter H, Deger A, Engh R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY17867 standard; Protein; 152 AA.
                       (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-USZ6086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 97.7
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 INIFTRLRTOKE 161
                                                                                                                            WPI; 1997-482043/45.
                                                                                                                                                  N-PSDB; AAT73194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken avidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-1999
                                                                                        Schmitt U;
                                                                                                                                                                                                                                   in assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY17867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avidin;
hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
AAY17867
      P<sub>P</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
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0
                                                                                                                                                                                                                                                                 fusion protein. This comprises Avidin mature peptide, a plant-noxious fusion protein. This comprises Avidin mature peptide, a plant-noxious protein. This comprises Avidin mature peptide, a plant-noxious protein. Gused to the PPI-I signal peptide. Transformation of plant genome with the vector encoding the fusion protein can produce pest resistance in plants, plant derived products and stored harvest material. Pests that can be controlled include, cotton bollworm, tropical army-worm, European corn-borer or red mitte, tobacco horn worm, loopers, rice stem borer, porina, cutworms, diamondback moth, potato tuber moth, codling moth, indian meal moth, gypsy moth, argentine stem weevil, grass-grubs, corn rockworm, rice and wheat weevils, maalworms, flour beetles, black field cricket, locusts, sawflies, Western flower thrips, Hessian flies or two-spotted mite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MESKFAHIIVFFLLATPFETLLARKESDGPEIPARKCSLTGKWTNDLGSNWTIGAVNSRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murray C, Markwick NP, Philip BA;
                                                                                                                                                                   New chimeric polypeptide and composition comprising the polypeptide useful for conferring pest resistance on plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptavidin; biotin; anti-interference reagent; detection; mutein; avidin; non-specific binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NGKEVLKTMWLLRSSVNDIGDDWKATRVGINIFTRLRTQKE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 845; DB 21; 100.0%; Pred. No. 3.6e-83;
(HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                 Example 2; Fig 8; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW29307 standard; Protein; 152
                                             Christeller JT, Sutherland PW,
Malone LA, Burgess EPJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..24
/label= signal
25..152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wild-type avidin protein.
                                                                                                         WPI; 2000-171244/15.
N-PSDB; AAZ49865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE19637718-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW29307;
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                                                                                                                                   The present invention describes a fibrinogen-converting enzyme fusion protein (FCE). The fusion protein is a multidomain protein comprising:

(a) a FCE; and (b) a first member of a binding pair, that is linked to the FCE chain: (i) directly by bonds utilizing the N-terminal amino groups, the C-terminal carboxy groups or side-chain functionalities;

(ii) Via a bifunctional linkage moiety linking the groups or functionalities; or (iii) by the first member be groups or member of the binding pair, where the second member of the binding pair is covalently attached to the first polypeptide chain. The FCE can be used in a method for producing fibrin. Fibrin is useful as a sealant in surgery to, e.g. reduce bleeding by sealing blood vessels, and tissues that have been dissected either in surgery or through wounding. The fusion protein allows for the removal of the fibrinogen converting enzyme from the fibrin sealant preparation via the binding of enzyme from the fibrin sealant preparation via the binding of strepteavidin to a biotin solid support. The present invention.
                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    30 PEIPARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avidin; biotin; neutravidin; ligand-binding molecule; cross-linked structure; polynucleotide delivery; DNA linking; biotin-avidin networked gene system; BANG system; DNA vaccine.
                                                                                                                                                                                                                                                                                                                                                                         Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "linked to a carbohydrate chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "this residue may also be Thr"
                                                                                                                                                                                                                                                                                                                                                                         Score 684; DB 20;
Pred. No. 7.6e-66;
                                                                                          A fibrinogen-converting enzyme fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of the avidin monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                  Disclosure; Page 27; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY30130 standard; peptide; 152 AA.
          (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                         80.98;
97.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28..107
                                 Cederholm-Williams SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 INIFTRLRTQKE 161
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                        WPI; 1999-385599/32
                                                                                                                                                                                                                                                                                                                                        152 AA;
                                                                    N-PSDB; AAX80197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                         Sednence
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY30130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
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tetramer, where each of the four monomer units binds to one biothn.

Biotin is complexed with a neutral avidin (neutravidin), and then
covalently coupled with polynucleotides, to exemplify the invention. The
specification describes a composition of complexes of polynucleotide
molecules covalently coupled to ligand moleties that are specifically
bound to ligand binding molecules to form a cross-linked structure.
The composition allows incorporation of diverse oligonucleotides or
polynucleotides into a single complex for concomitant delivery into the
same cell. The method and compositions provide a new way of linking DNA
molecules and are useful for gene over-expression and non-covalent
cloning. The new system is called biotin-avidin networked gene (BANG)
system. It is possible that the BANG system can be used to link multiple
gene complexes to elicit broader immune reactions, e.g. as DNA vaccines.
The BANG system can also be used as a cloning tool. The BANG system also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scavenger receptor class A; ScR; avidin; fusion protein; bovine; ECD; membrane-spanning domain; extracellular domain; biotin-binding activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents an avidin monomer. Avidin exists as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 NKRIQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 PEIPARKCSLTGKWTNDLGSNWTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cross-linked polynucleotide complexes, useful for cell-targeted polynucleotide delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine scavenger receptor class A (ScR)/avidin fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                       /note= "biotin binding occurs here"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 681; DB 20;
Pred. No. 1.6e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 40; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY03098 standard; Protein; 400 AA.
                                                                                                                                                                                                                                                                                                                      (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.68;
                                                                                                                                                                                                     99WO-US02673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 INIFTRLRTQKE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmids and vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-518369/43
Misc-difference 57
                                                                                                                                                                                                                                                                                                                                                                            D, Muller MT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-DEC-1999
                                                                                                                                                                                                     10-FEB-1999;
                                                                                                                                                                                                                                                             10-FEB-1998;
                                                                                WO9939744-A1
                                                                                                                                            12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY03098
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AAY03098
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and a mutant bacterial streptavidin, which are capable of generating stable dimers with reversible blotin binding activity. These can be used in signal transduction studies, protein purification and immunoassays. The present sequence is the chicken egg white avidin protein.
                                                                                                                                                                                                                                                           The present invention provides a mutant chicken egg white avidin protein
                                                                                                                                                                             Avidin and streptavidin mutants comprising tryptophan 110 and tryptophan 120 respectively, substituted by lysine for use in all known avidin/streptavidin-biotin systems and a purification process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chicken; egg white; avidin; bacterial streptavidin; mutant; mutein; dimer; biotin binding activity; protein purification; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                            34 ARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTINKRT
                                                                                                                                                                                                                                                                                                                                                                              DB 22, Length 128;
                                                                                                                              Laitinen OH;
                                                                                                                                                                                                                                                                                                                                                                            Score 670; DB 22
Pred. No. 2e-64;
1; MISMALCHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chicken egg white avidin W110K mutant.
                                                                                                                              Bayer EA, Wilchek M,
                                                                                                                                                                                                                                    Disclosure; Page 43; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB35271 standard; protein; 128 AA.
                                                                                                     RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD
                                                                            99US-0354097,
                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 79.3%;
Best Local Similarity 98.4%;
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUL-2000; 2000WO-US18959.
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                                                 .3-JUL-2000; 2000WO-US18959
                                                                                                                                                        WPI; 2001-147344/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dimer; biotin bindin siqual transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 TRLRTQKE 161
 WO200105977-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200105977-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gallus.
                                                                                                     (YEDA ) YEDA
                                                                            15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2001
                                                                                                                              Kulomaa MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2001
                          25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus
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                                                                                                                                                                                                                                                                                                                                                This invention describes a novel protein (A) which comprises a membrane-spanning domain and an extracellular domain (ECD), where the ECD comprises biotin-binding activity. Using the proteins or encoding nucleic acid molecules it is possible to target biotinylated molecules to specific sites in tissues. Molecules transpared in this way may be to exert their effects within or on the cell. This sequence represents a bouine scavenger receptor class A/avidin fusion protein which is used in
                                                                                                                                                                                                                                                                       New fusion proteins having an extracellular domain with biotin-binding activity, used to target biotinylated molecules to specific sites in
                                                                                                                                                                                                           Alrenne K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 arkcsltgkwtndlgsnmtigavnsrgeftgtyltavtatsneikesplhgtgntinkrt 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVGINIF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 ARKCSLTGKWTNDLGSNWTIGAVNSRGEFTGTVITAVTATSNEIKESPLHGTQNTINKRT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicken; egg white; avidin; bacterial streptavidin; mutant; mutein; dimer; biotin binding activity; protein purification; immunoassay; signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 400;
                                                                                                                                                                                                        Lehtolainen P, Marjomaki V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 678; DB 20;
Pred. No. 1.2e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.2%; Scur.
100.0%; Pred. No. 1.-
                                                                                                                                                                                                                                                                                                                           Claim 5, Page 21-23, 23pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                          the description of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 128
                                                                                                                                                                                                       Vla-Herttuala S, Kulomaa M,
                                                                                                                 99WO-GB00546
                                                                                                                                         98GB-0003757
                                                                                                                                                     98GB-0013653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chicken egg white avidin.
                                                                                                                                                                                 (EURO-) EUROGENE LID.
                                                                                                                                                                                                                                WPI; 1999-561345/47.
N-PSDB; AAZ09997.
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Best Local Similarity
Matches 128; conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus
                                                              409942577-A2
                                                                                                                23-FEB-1999;
                                                                                                                                         23-FEB-1998;
24-JUN-1998;
endocytosis
                                                                                      26-AUC-1999
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                                      Bos taurus.
                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                   tissues
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See also AAR56482-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skerra A,
                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                     AAW59217;
                   Sequence
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                                                                                                and a mutant bacterial streptavidin, which are capable of generating stable dimers with reversible biotin binding activity. These can be used in signal transduction studies, protein purification and immunoassays. The present sequence is the mutant chicken egg white avidin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of the ScFv pRAS110 and pRAS114 between HindIII and EcoRI site obtd. by PCR.
                                                                                       present invention provides a mutant chicken egg white avidin protein
                                  Avidin and streptavidin mutants comprising tryptophan 110 and tryptophan 120 respectively, substituted by lysine for use in all known avidin/streptavidin-biotin systems and a purification process
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                           9
                                                                                                                                                                                                          34 ARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAVTATSNEIKESPLHGTQNTINKRT 93
                                                                                                                                                                                                                    portion
                                                                                                                                                                                                                                                                                                                                                                                                                     Amplification; single chain variable region fusion protein; PCR
                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w cpds. comprising a targetting portion and a cytotoxic por
used esp. for treating mammals for destroying target cells.
intic. tumour cells
                                                                                                                                                                       Length 128;
                                                                                                                                                                                        Indels
                                                                                                                                                                     Score 656; DB 22;
Pred. No. 6.3e-63;
1; Mismatches 2;
Laitinen OH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spooner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMCR ) IMPERIAL CANCER RES TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                              AAR56485 standard; Protein; 402 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 11; 114pp; English.
Wilchek M,
                                                                      Disclosure; Page 45; 49pp; English
                                                                                                                                                                      Query Match 77.6%;
Best Local Similarity 97.7%;
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93GB-0000686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-GB00087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Epenetos AA,
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   ScFV pRAS110 and pRAS114
Bayer EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-248907/30.
                 WPI; 2001-147344/15
                                                                                                                                             128 AA;
                                                                                                                                                                                                                                                                                TRLRTQKE 161
                                                                                                                                                                                                                                                                                                  trlrtqke 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ70661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deonarain M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9415644-A.
Kulomaa MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                AAR56485;
                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              partic.
                                                                                                                                                                                                                                                                                154
                                                                                                                                                                                                                                                                                                  121
                                                                                       The
                                                                                                                                                                                                                                                                                                                                      AAR56485
δ
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This sequence represents a mutant streptavidin protein isolated from Streptomyces avidinii where the residues ESAV at position 44-47 of the mature wild type sequence are replaced by VTAR. This sequence is used to produce mutants which are used in a method to assay the binding affinity of streptavidin mutants. These mutants have a mutation within the amino acid (aa) region 44-53 of the wild-type protein show a higher binding affinity than the wild-type for peptide ligands that include the sequence of formula Trp-X-His-Pro-Gln-Phe-Y-2 where X=any as; Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Wild type ESAV is replaced by VTAR. Numbering is from the start of the mature protein"
                                                                                                                                                                                                                                                    85 TQNTINKRTQPTFGFTVNWK----FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDI 139
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptavidin mutants with higher binding affinity for peptide
ligands - have mutation in amino acid region 44-53, used to isolate,
purify or determine fusion proteins including these ligands
                                                                                                                                                                 GPEIPA - - - RKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAV -TATSNEIKESPLHG
                                                                            16;
                    Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptavidin; ligand; binding affinity; mutant; isolation; purification; recover; immobilise.
                                                                            Indels
                                                                         57;
              ; Score 148; DB 15;
; Pred. No. 1.8e-07;
18; Mismatches 57;

 avidinii streptavidin mutant protein #1.

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68.71
/label= vTAR68ESAV
/note= "Wild type ESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW59217 standard; Protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page -; 21pp; German.
                 17.5%;
34.1%;
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380 anawkstlvqhdtftkvk 397
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                                                                                                                                                                                                                                                                                                                                                                 140 GDDWKATRVGINIFTRLR 157
Query Match
Best Local Similarity 34.1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces avidinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-218868/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Voss S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV34715.
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16.9%; Scc
32.3%; Pre
tive 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88WO-GB00831,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIO-TECHN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                         145 ATRVGINIFTRLR 157
                                                                                                                                                                                                                                                            :| || : ||::
122 stlvghdtftkvk 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 ATRVGINIFTRLR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biotin; chimeric gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1989-130040/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
                                   Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAN90755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRBI-) BRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-ocr-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO8903422-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-1989
                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edwards RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                              AAP93531;
                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                               AAP93531
                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                         7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a mutant chicken egg white avidin protein and a mutant bacterial streptavidin, which are capable of generating stable dimers with reversible blottin binding activity, These can be used in signal transduction studies, protein purification and immunoassays. The present sequence is the Streptomyces avidinii streptavidin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avidin and streptavidin mutants comprising tryptophan 110 and tryptophan 120 respectively, substituted by lysine for use in all known avidin/streptavidin-biotin systems and a purification process
and Z are both Gly, or Y = Glu and Z = Arg or Lys. Recombinant streptavidin mutants can be used to isolate, purify and determine proteins or to determine/recover substances that contain streptavidin-binding groups. Such compounds may also be used to immobilise fusions on microtitre plates, microbeads or sensor chips. NOTE: This sequence does not appear in the specification but has been constructed from the wild-type Streptavidin sequence represented in AAV34714.
                                                                                                                                                                                                                                                                                                                                                                                90 NKRTQPTFGFTVNWK----FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWK 144
                                                                                                                                                                                                                                                                                          31 EIDARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITA-VTATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                            33 qvsaaeagitgtwynqlgstfivta-gadgaltgtyvtargnaesryvltgrydsapatd 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chicken; egg white; avidin; bacterial streptavidin; mutant; mutein; dimer; blotin binding activity; protein purification; immunoassay;
                                                                                                                                                                                                                        DB 19; Length 183;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                         57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laitinen OH;
                                                                                                                                                                                                                      Score 145.5; DB ... Pred. No. 1.1e-07. D. Mismatches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB35270 standard; protein; 159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces avidinii streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Σ̈́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 44; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilchek
                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                        17.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0354097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUL-2000; 2000WO-US18959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bayer EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| || : ||:::
146 stlvghdtftkvk 158
                                                                                                                                                                                                                                                                                                                                                                                                                                145 ATRVGINIFTRLR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dimer; biotin bindin
signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-147344/15.
                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                      183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200105977-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kulomaa MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB35270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The synthetic gene is constructed from 24 oligomers (BBZ14-BBZ37) which were synthesised by automated phosphoramidite chemistry. Apart from Met-1, it has the same sequence as natural mature streptovidin protect produced by Streptomyces avidinii.
                                                                                                                                                                                                                                                           gsgt--algwtvawknnyrnahsattwsggyv---ggaearintgwlltsgtte-anawk 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 NKRTOPTFCFTVNWK----FSESTTVFTCOCFIDRNGKEV-LKTMWLLRSSVNDIGDDWK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKRTQPTFGFTVNWK----FSESTTVFTGQCFIDRNCKEV-LKTMWLLRSSVNDIGDDWK 144
                                                  Gaps
                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 EIPARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIPARKCSLTCKWTNDLCSNMTICAVNSRCEFTCTYITAV-TATSNEIKESPLHGTQNTI 89
                                                                                                                                                     9 qvsaacagitgtwynqlgstfivta-gadgaltgtyesavgnaesryvltgrydsapatd
                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 160;
  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptavidin; synthetic gene; Streptomyces avidinii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising hybrid gene encoding fusion protein with biotin-binding activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mature Streptavidin as encoded by a synthetic gene.
Score 142.5; DB 22;
Pred. NO. 2e-07;
); Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence encoding streptavidin and vector
                                                                                                                                                                                                                                     =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP93531 standard; protein; 160 AA.
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:| || : ||::: 123 stlvqhdtftkvk 135

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us-09-743-690-7.rag

124 stlvghdtftkvk 136

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Plant somatic tissue degeneration; plant essential factor; depletion; viability; prost gene; plant development; plant morphology; flower; fruit plant.
                                                                                                                                               Streptomyces avidinii prost protein.
                                  AAY80514 standard; Protein; 162 AA.
                                                                                                                                                                                                                                                         Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AGRI-) AGRIC RES ORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kapulnik Y, Ginzberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-195402/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ91075
                                                                                                                                                                                                                                                                                              WO200007427-A2.
                                                                                                                                                                                                                                                                                                                                                                      30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-1998;
                                                                                                            06-JUN-2000
                                                                                                                                                                                                                                                                                                                                  17-FEB-2000
                                                                      AAY80514;
RESULT 13
                   AAY80514
                                                                      The invention relates to a method of effecting degeneration of a somatic plant tissue by expressing a heterologous protein capable of binding a plant tissue by factor (PEF), in somatic plant tissue cells, where heterologous protein expression causes depletion of the PEF so the plant viability is maintained, while simultaneous degeneration of the somatic plant tissue is effected. This sequence represents the Streptomyces avidinii mprost protein as an example of a heterologous protein introduced into the plants. The methods can provide for the selective and optionally reversible cell degeneration in somatic plant tissue. They can be used for artificially controlling plant development and morphology. They can be used e.g. to decrease the number of flowers in finite producing plants so as to increase the number of fruits which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, such as decreasing the number of flowers present to increase the number of
                                                                                                                                                                                            Plant somatic tissue degeneration; plant essential factor; depletion; viability; mprost gene; plant development; plant morphology; flower; fruit plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.9%; Score 142.5;
ilarity 32.3%; Pred. No. 2e-
Conservative 20; Mismatches
                                                                                                                                                            Streptomyces avidinii mprost protein
                                               AAY80515 standard; Protein; 161 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examples; Page 87; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     99WO-IL00420.
                                                                                                                                                                                                                                                                                                                                                                                                                          98IL-0125632.
                                                                                                                        06-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kapulnik Y, Ginzberg I;
                                                                                                                                                                                                                                                                         Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AGRI-) AGRIC RES ORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-195402/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ91076
                                                                                                                                                                                                                                                                                                           WO200007427-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reach maturity
                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                               17-FEB-2000
                                                                                     AAY80515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
               12
                                AAY80515
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99WO-IL00420.

(first entry)

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7
                                                                                                                                                                                                            The invention relates to a method of effecting degeneration of a somatic plant tissue by expressing a heterologous protein capable of binding a plant tissue by expressing a heterologous protein capable of binding a heterologous protein expression causes depletion of the PEF so the plant viability is maintained, while simultaneous degeneration of the somatic plant tissue is effected. This sequence represents the Streptomyces avidini prost protein as an example of a heterologous protein introduced into the plants. The methods can provide for the selective and optionally reversible cell degeneration in somatic plant tissue. They can be used for artificially controlling plant development and morphology. They can be used e.g. to decrease the number of flowers in fruit producing plants so as to increase the number of fruits which reach maturity.
Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, such as decreasing the number of flowers present to increase the number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 NKRTQPTFGFTVNWK----FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIPARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.9%; Score 142.5; DB 21; Length 162; 32.3%; Pred. No. 2e-07; ive 20; Mismatches 57; Indels 13;
                                                                                                                                                           Examples; Page 86; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| || : ||:::
125 stlvghdtftkvk 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 ATRVGINIFTRLR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                             fruit
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Indels

Pred. No. 2e-07;); Mismatches 57;

Local Similarity

43;

Best Loca Matches 31

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145 ATRVGINIFTRLR 157

EIPARKCSLIGKWTNDLGSNMTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHGTQNTI 89 11 qvsaaeagitgtwynqlgstfivta-gadgaltgtyesavgnaesryvltgrydsapatd

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Search completed: September 17, 2002, 15:42:04 JOD time: 265 sec
                                                             24-FEB-1987;
                                                                               24-FEB-1986;
                         WOB705026-A
                                           27-AUG-1987
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
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                                                                                                                                                                                                                                                                                                                                                                                                                                1:
                                                                                                                                                                                                                                                                                          naving an antibody binding site and a sequence for biological activity, ion sequestering or binding to a solid support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 NKRIQPIFGFIV,WWK----FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 EIPARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHGTQNTI 89
                                                                                                                                                                                                                                                                                                                                     Multi-functional biosynthetic protein comprising single Chain BABS and streptavidin protein trailer linked via a spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 163;
                                                                                                Biosynthetic Antibody Binding site (BABS); variable domain; anti-CEA monoclonal antibody; streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptavidin; N-terminal; fusion gene; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                                                                                                                                                                                                                                                                                                             16.9%; SCOIE 142.5; DB 9; 32.3%; Pred. No. 2.1e-07; tive 20; Mismatches 57;
                                                                                Biosynthetic protein with streptavidin trailer.
                                                                                                                                                                                                                                                                                  Recombinant multifunctional protein
                        AAP80160 standard; protein; 163 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP70492 standard; protein; 182 AA.
                                                                                                                                                                                                                   (CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                    Disclosure; ; 115pp; English
                                                                                                                                                                                                   87US-0052800.
                                                                                                                                                                                 88WO-US01737
                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                 See also AAN80171-N80192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| || : ||::
126 stlvghdtftkvk 138
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                                                                                                                                                                                                                                       Oppermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptavidin sequence
                                                                                                                                                                                                                                                        WPI; 1988-353928/49.
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   163 AA;
                                                                                                                                                                                                                                                                 N-PSDB; AAN80186.
                                                                                                                                                                                 19-MAY-1988;
                                                                                                                                                                                                   21-MAY-1987;
                                                             13-OCT-1990
                                                                                                                                               WO8809344-A
                                                                                                                                                                01-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                      Huston JS,
                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP70492;
                                           AAP80160;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
         14
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The sequence is that of streptavidin from S.avidinil. Streptavidin may be expressed from a fusion gene comprising its coding gene and DNA encoding a target protein of interes, where he streptavidin has binding sites for biotin or deriv. The streptavidin has 4 binding sites free for biotin, and is produced free of biotin and is produced free of biotin site-directed mutagenesis. The fused gene may also be produced by site-directed mutagenesis. The fused gene may be used to produce labelled, chemically-modified proteins in vivo, and to isolate proteins when only the sequence of the gene is known.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 NKRTOPTFGFTVNWK----FSESTTVFTGQCFIDRNGKEY-LKTMWLLRSSVNDIGDDWK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 EIPARKCSLTGKWINDLGSNWTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHCTONTI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding Streptavidin - obtd, by restriction endo-nuclease digestion of chromosomal DNA of Streptomyces avidinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.9%; Score 142.5; DB 8; 32.3%; Pred. No. 2.4e-07; Live 20; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 3; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Garana C;
                                                                                                                                                                                87WO-US00397
                                                                                                                                                                                                                                         86US-0833324
                                                                                                                                                                                                                                                                                                  (UYCO-) COLUMBIA UNIV N Y. (UYNY-) UNIV NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 32.3
nes 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 ATRVGINIFTRLR 157
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stlvghdtftkvk 157
Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1987-250198/35.
N-PSDB; AAN70810.
                                                                                                                                                                                                                                                                                                                                                                                                Cantor CR, Axel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 AA;
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